

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 32.5171 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	34	13	AAR22296	Human parathyroid
2	34	100.0	34	23	AAU73030	Parathyroid hormon
3	30	88.2	30	23	AAU73053	Parathyroid hormon
4	30	88.2	35	23	AAU73174	Parathyroid hormon
5	24	70.6	34	18	AAW08108	Human parathyroid
6	23	67.6	28	13	AAR22064	Modified hPTH(7-34
7	23	67.6	28	21	ABJ10776	Human parathyroid
8	23	67.6	28	23	AAE23734	Human parathyroid
9	23	67.6	28	23	AAU73044	Parathyroid hormon
10	23	67.6	30	23	AAE23752	Human parathyroid
11	23	67.6	32	21	AAB07468	Antigenic peptide
12	23	67.6	32	23	AAE23735	Human parathyroid
13	23	67.6	34	4	AAP30022	Human parathyroid-
14	23	67.6	34	6	AAP50377	[Met(O)8,18]hPTH-(
15	23	67.6	34	7	AAP60031	Sequence of the fi
16	23	67.6	34	11	AAR07919	Human parathyroid
17	23	67.6	34	13	AAR22283	Parathyroid hormon
18	23	67.6	34	13	AAR22292	Human parathyroid
19	23	67.6	34	13	AAR22293	Human parathyroid
20	23	67.6	34	13	AAR22294	Human parathyroid
21	23	67.6	34	14	AAR41549	[D-Ser3]hPTH (1-34
22	23	67.6	34	14	AAR41550	[D-Ala3]hPTH (1-34
23	23	67.6	34	14	AAR41570	[Gln25]hPTH (1-34)
24	23	67.6	34	15	AAR49697	Sequence of varian
25	23	67.6	34	15	AAR49698	Sequence of varian
26	23	67.6	34	15	AAR58291	[Lys(For)26, Lys(F
27	23	67.6	34	15	AAR58228	[D-Asp30]-hPTH(1-3
28	23	67.6	34	15	AAR58016	N-alpha-Isopropyl-
29	23	67.6	34	15	AAR58017	[Lys(N-epsilon-Iso
30	23	67.6	34	15	AAR55724	Parathormone N-ter
31	23	67.6	34	16	AAR74521	Human parathyroid
32	23	67.6	34	17	AAW99449	Human parathyroid
33	23	67.6	34	17	AAW15812	[Trp(10)]-hPTH(1-3
34	23	67.6	34	17	AAR99978	Human parathyroid
35	23	67.6	34	17	AAR98951	Target peptide (PT
36	23	67.6	34	17	AAR98966	PTH(1-34). Not sp
37	23	67.6	34	17	AAR88835	Human parathyroid
38	23	67.6	34	18	AAW24273	Wild type parathyr
39	23	67.6	34	18	AAW08120	Human PTH derivati
40	23	67.6	34	18	AAW08109	Human parathyroid
41	23	67.6	34	18	AAW08113	Human PTH derivati
42	23	67.6	34	18	AAW08114	Human PTH derivati
43	23	67.6	34	18	AAW08117	Human PTH derivati
44	23	67.6	34	18	AAW08118	Human PTH derivati
45	23	67.6	34	18	AAW08119	Human PTH derivati
46	23	67.6	34	18	AAW19994	Cyclised human par
47	23	67.6	34	18	AAW20000	Cyclised human par
48	23	67.6	34	18	AAW20006	Cyclised human par
49	23	67.6	34	18	AAW17941	Human parathyroid
50	23	67.6	34	18	AAW17943	Human parathyroid

51	23	67.6	34	18	AAW17939	Human parathyroid
52	23	67.6	34	18	AAW17957	Human parathyroid
53	23	67.6	34	18	AAW01609	Parathyroid hormon
54	23	67.6	34	19	AAW67274	Parathyroid hormon
55	23	67.6	34	19	AAW67276	Parathyroid hormon
56	23	67.6	34	19	AAW67278	Parathyroid hormon
57	23	67.6	34	19	AAW67290	Parathyroid hormon
58	23	67.6	34	19	AAW67291	Parathyroid hormon
59	23	67.6	34	19	AAW67299	Parathyroid hormon
60	23	67.6	34	19	AAW61658	Parathyroid hormon
61	23	67.6	34	19	AAW65975	Human parathyroid
62	23	67.6	34	20	AAV50593	Resin bound cyclic
63	23	67.6	34	20	AAV17752	Human parathyroid
64	23	67.6	34	20	AAV14151	Human parathyroid
65	23	67.6	34	20	AAV02579	N-terminal 34 resi
66	23	67.6	34	20	AAW81871	Human PTH N-termin
67	23	67.6	34	21	ABJ10706	Human parathyroid
68	23	67.6	34	21	ABJ10712	Human parathyroid
69	23	67.6	34	21	ABJ10713	Human parathyroid
70	23	67.6	34	21	ABJ10714	Human parathyroid
71	23	67.6	34	21	ABJ10717	Human parathyroid
72	23	67.6	34	21	ABJ10719	Human parathyroid
73	23	67.6	34	21	ABJ10722	Human parathyroid
74	23	67.6	34	21	ABJ10724	Human parathyroid
75	23	67.6	34	21	ABJ10727	Human parathyroid
76	23	67.6	34	21	ABJ10729	Human parathyroid
77	23	67.6	34	21	ABJ10730	Human parathyroid
78	23	67.6	34	21	ABJ10733	Human parathyroid
79	23	67.6	34	21	ABJ10736	Human parathyroid
80	23	67.6	34	21	ABJ10737	Human parathyroid
81	23	67.6	34	21	ABJ10769	Human parathyroid
82	23	67.6	34	21	AAB07454	Amino acids 1-34 o
83	23	67.6	34	21	AAV98010	Human amino-termin
84	23	67.6	34	21	AAV98011	Human amino-termin
85	23	67.6	34	21	AAV98014	Human amino-termin
86	23	67.6	34	21	AAV98017	Human amino-termin
87	23	67.6	34	21	AAV82631	Human parathyroid
88	23	67.6	34	21	AAV68763	Amino acids 1-34 o
89	23	67.6	34	22	AAB84778	Native rat parathy
90	23	67.6	34	22	AAB96898	Human parathyroid
91	23	67.6	34	22	AAB81079	Human parathyroid
92	23	67.6	34	22	AAB91098	Parathyroid hormon
93	23	67.6	34	22	AAB91113	Parathyroid hormon
94	23	67.6	34	22	AAB61638	Peptide #1 that ca
95	23	67.6	34	23	ABJ05328	Human PTH(1-34) pe
96	23	67.6	34	23	AAE23727	Human parathyroid
97	23	67.6	34	23	AAE23728	Human parathyroid
98	23	67.6	34	23	ABB06329	Human parathyroid
99	23	67.6	34	23	ABB08595	C-terminal truncat
100	23	67.6	34	23	AAE18395	Human PTH peptide
101	23	67.6	34	23	AAE18399	Human PTH peptide
102	23	67.6	34	23	ABB07147	Parathyroid hormon
103	23	67.6	34	23	AAU73028	Parathyroid hormon
104	23	67.6	34	23	AAU73029	Parathyroid hormon
105	23	67.6	34	23	AAU73032	Parathyroid hormon
106	23	67.6	34	24	ABP71500	Human parathyroid
107	23	67.6	34	24	ABG74235	Human parathyroid

165	23	67.6	36	15	AAR58197	[Ala3]-hPTH(1-36)-
166	23	67.6	36	15	AAR58198	[D-Ser3]-hPTH(1-36
167	23	67.6	36	15	AAR58199	[D-Glu4]-hPTH(1-36
168	23	67.6	36	15	AAR58200	[D-His9]-hPTH(1-36
169	23	67.6	36	15	AAR58201	[Ala10]-hPTH(1-36)
170	23	67.6	36	15	AAR58202	[D-Asn10]-hPTH(1-3
171	23	67.6	36	15	AAR58210	[D-His14]-hPTH(1-3
172	23	67.6	36	15	AAR58211	[D-Asn16]-hPTH(1-3
173	23	67.6	36	15	AAR58213	[D-Ser17]-hPTH(1-3
174	23	67.6	36	15	AAR58215	[D-Glu19]-hPTH(1-3
175	23	67.6	36	15	AAR58220	[D-Lys26]-hPTH(1-3
176	23	67.6	36	15	AAR58169	[D-Pro1]-hPTH(1-36
177	23	67.6	36	15	AAR58170	[Nva1]-hPTH(1-36)-
178	23	67.6	36	15	AAR58171	[N-Me-Ser1]-hPTH(1
179	23	67.6	36	15	AAR58172	[Indole-2-carboxyl
180	23	67.6	36	15	AAR58173	[Indole-3-carboxyl
181	23	67.6	36	15	AAR58174	[Pyridine-3-carbox
182	23	67.6	36	15	AAR58175	[Pyridine-2-carbox
183	23	67.6	36	15	AAR58176	[Hexahydropyridazi
184	23	67.6	36	15	AAR58177	[Morpholine-2-carb
185	23	67.6	36	15	AAR58178	[Pro1]-hPTH(1-36)-
186	23	67.6	36	15	AAR58179	[Leu1]-hPTH(1-36)-
187	23	67.6	36	15	AAR58180	[Ile1]-hPTH(1-36)-
188	23	67.6	36	15	AAR58182	[Nva8]-hPTH(1-36)-
189	23	67.6	36	15	AAR58026	N-alpha-methyl [Ala
190	23	67.6	36	15	AAR58168	[1-amino-cyclopent
191	23	67.6	37	12	AAR11882	Parathyroid hormon
192	23	67.6	37	13	AAR24778	hPTH(1-37)-amide/e
193	23	67.6	37	15	AAR58244	[Ala0]-hPTH(1-36)-
194	23	67.6	37	15	AAR58245	[Pro0]-hPTH(1-36)-
195	23	67.6	37	22	AAB86226	Human parathyroid
196	23	67.6	37	22	AAB86229	Human parathyroid
197	23	67.6	37	23	ABB82203	Human parathyroid
198	23	67.6	37	23	AAU73027	Parathyroid hormon
199	23	67.6	38	15	AAR58269	[Leu8]-hPTH(1-38)-
200	23	67.6	38	15	AAR58282	[Trp (SO2Pmc) 23]-hP
201	23	67.6	38	15	AAR58283	[Trp (Pmc) 23]-hPTH(
202	23	67.6	38	15	AAR58018	Isopropyl-[Lys (Iso
203	23	67.6	38	15	AAR58019	N-alpha-methyl [Ala
204	23	67.6	38	15	AAR58022	[Ile1]-hPTH(1-38)-
205	23	67.6	38	15	AAR58023	[Ala1, Abu2 or Nva2
206	23	67.6	38	15	AAR58024	[Ala1, Ile2]-hPTH(1
207	23	67.6	38	15	AAR58028	[Thr1]-hPTH(1-38)-
208	23	67.6	38	15	AAR58029	[Leu1]-hPTH(1-38)-
209	23	67.6	38	15	AAR58030	[Abu1 or Gabal]-hP
210	23	67.6	38	15	AAR54234	PTH N-terminal. S
211	23	67.6	38	17	AAR98958	Target peptide (PT
212	23	67.6	38	20	AAV02580	N-terminal 38 resi
213	23	67.6	38	22	AAB91101	Parathyroid hormon
214	23	67.6	38	23	AAE23729	Human parathyroid
215	23	67.6	38	23	AAE18400	Human PTH peptide
216	23	67.6	38	23	AAU73026	Parathyroid hormon
217	22	64.7	28	13	AAR22065	Modified [Tyr_34]h
218	22	64.7	31	5	AAP40760	Human parathyroid
219	22	64.7	32	5	AAP40427	Parathyroid antago
220	22	64.7	33	17	AAR88841	Human parathyroid
221	22	64.7	33	21	AAV98012	Human amino-termin

108	23	67.6	35	22	AAB91112	Parathyroid hormon
109	23	67.6	35	23	AAU73172	Parathyroid hormon
110	23	67.6	35	23	AAU73173	Parathyroid hormon
111	23	67.6	36	12	AAR15842	Human parathyroid
112	23	67.6	36	13	AAR23995	Human paprthyroid
113	23	67.6	36	14	AAR39450	Ser-Val-(hPTH 3-35
114	23	67.6	36	15	AAR58286	[D-Leu24]-hPTH(1-3
115	23	67.6	36	15	AAR58292	[D-Lys27]-hPTH(1-3
116	23	67.6	36	15	AAR58293	[D-Leu28]-hPTH(1-3
117	23	67.6	36	15	AAR58294	[D-Phe34]-hPTH(1-3
118	23	67.6	36	15	AAR58295	[D-Val35]-hPTH(1-3
119	23	67.6	36	15	AAR58296	[Ala35]-hPTH(1-36)
120	23	67.6	36	15	AAR58297	[Pro35]-hPTH(1-36)
121	23	67.6	36	15	AAR58298	[NMeVal35]-hPTH(1-
122	23	67.6	36	15	AAR58299	[Thr35,Ala36]-hPTH
123	23	67.6	36	15	AAR58300	[D-Ala36]-hPTH(1-3
124	23	67.6	36	15	AAR58301	[NMeAla36]-hPTH(1-
125	23	67.6	36	15	AAR58254	[4-aminosalicylic
126	23	67.6	36	15	AAR58255	[TMSA1]-hPTH(1-36)
127	23	67.6	36	15	AAR58256	[Phe1]-hPTH(1-36)-
128	23	67.6	36	15	AAR58257	[Propargylglycin1]
129	23	67.6	36	15	AAR58259	[aBU2]-hPTH(1-36)-
130	23	67.6	36	15	AAR58260	[D-Val2]-hPTH(1-36
131	23	67.6	36	15	AAR58261	[Tert. Leu]-hPTH(1-
132	23	67.6	36	15	AAR58262	[Ala1]-hPTH(1-36)-
133	23	67.6	36	15	AAR58263	[D-Ile5]-hPTH(1-36
134	23	67.6	36	15	AAR58264	[D-Gln6]-hPTH(1-36
135	23	67.6	36	15	AAR58265	[D-Leu7]-hPTH(1-36
136	23	67.6	36	15	AAR58266	[Nle8]-hPTH(1-36)-
137	23	67.6	36	15	AAR58267	[Phe8]-hPTH(1-36)-
138	23	67.6	36	15	AAR58268	[Cha8]-hPTH(1-36)-
139	23	67.6	36	15	AAR58270	[D-Leu11]-hPTH(1-3
140	23	67.6	36	15	AAR58271	[Ala11]-hPTH(1-36)
141	23	67.6	36	15	AAR58272	[D-Lys13]-hPTH(1-3
142	23	67.6	36	15	AAR58273	[D-Leu15]-hPTH(1-3
143	23	67.6	36	15	AAR58276	[Met(O2)18]-hPTH(1
144	23	67.6	36	15	AAR58278	[D-Met18]-hPTH(1-3
145	23	67.6	36	15	AAR58280	[D-Arg20]-hPTH(1-3
146	23	67.6	36	15	AAR58281	[D-Val21]-hPTH(1-3
147	23	67.6	36	15	AAR58284	[D-Trp23]-hPTH(1-3
148	23	67.6	36	15	AAR58227	[D-Gln29]-hPTH(1-3
149	23	67.6	36	15	AAR58230	[D-Val31]-hPTH(1-3
150	23	67.6	36	15	AAR58233	[D-His32]-hPTH(1-3
151	23	67.6	36	15	AAR58235	[D-Asn33]-hPTH(1-3
152	23	67.6	36	15	AAR58237	[NMePhe34]-hPTH(1-
153	23	67.6	36	15	AAR58238	[D-Asp30]-hPTH(1-3
154	23	67.6	36	15	AAR58242	[Lys(Isopropyl)13]
155	23	67.6	36	15	AAR58243	Propargyl-[A1]-hPT
156	23	67.6	36	15	AAR58246	Acetyl-hPTH(1-36)-
157	23	67.6	36	15	AAR58247	[Hyp1]-hPTH(1-36)-
158	23	67.6	36	15	AAR58248	N-Dimethyl-[Ala1]-
159	23	67.6	36	15	AAR58249	[D-Ser1]-hPTH(1-36
160	23	67.6	36	15	AAR58250	[Lys(For)1]-hPTH(1
161	23	67.6	36	15	AAR58251	[D-glyceric acid1]
162	23	67.6	36	15	AAR58252	[Asn1]-hPTH(1-36)-
163	23	67.6	36	15	AAR58253	[4-aminobenzoic ac
164	23	67.6	36	15	AAR58196	[D-Phe34, D-Ala36]

222	22	64.7	33	21	AAAY98015	Human amino-termin
223	22	64.7	33	21	AAAY98018	Human amino-termin
224	22	64.7	34	11	AAR07922	Human parathyroid
225	22	64.7	34	11	AAR08300	Human parathyroid
226	22	64.7	34	15	AAR58193	[L8,D10,K11,T33,A3
227	22	64.7	34	15	AAR58194	[A1,H5,L8,D10,K11,
228	22	64.7	34	18	AAW08121	Human PTH derivati
229	22	64.7	34	18	AAW08115	Human PTH derivati
230	22	64.7	34	18	AAW08116	Human PTH derivati
231	22	64.7	34	18	AAW17955	Human parathyroid
232	22	64.7	34	18	AAW17959	Human parathyroid
233	22	64.7	34	19	AAW48392	Human parathyroid
234	22	64.7	34	21	ABJ10772	Human parathyroid
235	22	64.7	34	21	ABJ10773	Human parathyroid
236	22	64.7	34	22	AAB96929	Human parathyroid
237	22	64.7	36	15	AAR58191	[Ala34]-hPTH(1-36)
238	22	64.7	36	15	AAR58203	[Ala12]-hPTH(1-36)
239	22	64.7	38	3	AAP20248	Parathyroid hormon
240	22	64.7	38	15	AAR58089	[Arg12]-hPTH(1-38)
241	22	64.7	38	15	AAR58090	[Ser12]-hPTH(1-38)
242	21	61.8	28	13	AAR22066	Modified [D-Trp_12
243	21	61.8	32	17	AAR88840	Human parathyroid
244	21	61.8	34	11	AAR08303	Human parathyroid
245	21	61.8	34	15	AAR58181	[Thr33, Ala34]-hPT
246	21	61.8	34	18	AAW08112	Human PTH derivati
247	21	61.8	34	19	AAW42614	Human parathyroid
248	21	61.8	34	22	AAB96893	Rat parathyroid ho
249	21	61.8	34	22	AAB96930	Rat parathyroid ho
250	21	61.8	36	15	AAR58236	[Ala33]-hPTH(1-36)
251	21	61.8	36	15	AAR58204	[Gln13]-hPTH(1-36)
252	21	61.8	36	15	AAR58205	[His13]-hPTH(1-36)
253	21	61.8	36	15	AAR58206	[Leu13]-hPTH(1-36)
254	21	61.8	36	15	AAR58207	[Ala13]-hPTH(1-36)
255	21	61.8	38	15	AAR58161	[Pro3,Thr33]-hPTH(
256	21	61.8	38	15	AAR58162	[Arg33]-hPTH(1-38)
257	21	61.8	38	15	AAR58163	[Pro33]-hPTH(1-38)
258	21	61.8	38	15	AAR58164	[Asp33]-hPTH(1-38)
259	21	61.8	38	15	AAR58165	[Ile33]-hPTH(1-38)
260	21	61.8	38	15	AAR58166	[Lys33]-hPTH(1-38)
261	21	61.8	38	15	AAR58075	[Ser33]-hPTH(1-38)
262	21	61.8	38	15	AAR58076	[Thr33]-hPTH(1-38)
263	21	61.8	38	15	AAR58077	[Leu33]-hPTH(1-38)
264	21	61.8	38	15	AAR58078	[Gly33]-hPTH(1-38)
265	21	61.8	38	15	AAR58084	[Gln33]-hPTH(1-38)
266	21	61.8	38	15	AAR58091	[Cys13]-hPTH(1-38)
267	21	61.8	38	15	AAR58092	[Ile13]-hPTH(1-38)
268	21	61.8	38	15	AAR58093	[Asn13]-hPTH(1-38)
269	21	61.8	38	15	AAR58094	[Trp13]-hPTH(1-38)
270	21	61.8	38	15	AAR58095	[Asp13]-hPTH(1-38)
271	21	61.8	38	15	AAR58096	[Val13]-hPTH(1-38)
272	21	61.8	38	15	AAR58097	[Thr13]-hPTH(1-38)
273	21	61.8	38	15	AAR58098	[Ser13]-hPTH(1-38)
274	21	61.8	38	15	AAR58099	[Tyr13]-hPTH(1-38)
275	21	61.8	38	15	AAR58100	[Met13]-hPTH(1-38)
276	21	61.8	38	15	AAR58101	[Gln13]-hPTH(1-38)
277	21	61.8	38	15	AAR58102	[Leu13]-hPTH(1-38)
278	21	61.8	38	15	AAR58103	[Ala13]-hPTH(1-38)

279	21	61.8	38	15	AAR58104	[Gly13]-hPTH(1-38)
280	20	58.8	30	6	AAP50665	Human parathyroid
281	20	58.8	31	17	AAR88830	Human parathyroid
282	20	58.8	31	19	AAW42059	Human parathyroid
283	20	58.8	31	19	AAW42051	Human parathyroid
284	20	58.8	31	20	AAV02578	N-terminal 31 resi
285	20	58.8	31	22	AAB81080	Human parathyroid
286	20	58.8	31	22	AAB91097	Parathyroid hormon
287	20	58.8	31	23	AAE23720	Human parathyroid
288	20	58.8	31	23	AAU73039	Parathyroid hormon
289	20	58.8	32	23	AAU73176	Parathyroid hormon
290	20	58.8	34	15	AAR58232	[Lys32]-hPTH(1-34)
291	20	58.8	34	18	AAW08129	Human PTH derivati
292	20	58.8	34	22	AAB84771	Parathyroid hormon
293	20	58.8	34	22	AAB84826	Parathyroid hormon
294	20	58.8	34	22	AAB96916	Parathyroid hormon
295	20	58.8	34	22	AAB96919	Parathyroid hormon
296	20	58.8	36	15	AAR58234	[Ala32]-hPTH(1-36)
297	20	58.8	36	15	AAR58209	[Ala14]-hPTH(1-36)
298	20	58.8	38	15	AAR58037	[Ser14]-hPTH(1-38)
299	20	58.8	38	15	AAR58105	[Val14]-hPTH(1-38)
300	20	58.8	38	15	AAR58106	[Ala14]-hPTH(1-38)
301	20	58.8	38	15	AAR58107	[Lys14]-hPTH(1-38)
302	20	58.8	38	15	AAR58108	[Arg14]-hPTH(1-38)
303	20	58.8	38	15	AAR58109	[Thr14]-hPTH(1-38)
304	20	58.8	38	15	AAR58110	[Ile14]-hPTH(1-38)
305	20	58.8	38	15	AAR58111	[Tyr14]-hPTH(1-38)
306	19	55.9	30	17	AAR88832	Human parathyroid
307	19	55.9	30	23	AAU73051	Parathyroid hormon
308	19	55.9	30	23	AAU73052	Parathyroid hormon
309	19	55.9	30	23	AAU73055	Parathyroid hormon
310	19	55.9	31	23	AAU73177	Parathyroid hormon
311	19	55.9	34	18	AAW17942	Human parathyroid
312	19	55.9	34	18	AAW17948	Human parathyroid
313	19	55.9	34	18	AAW17968	Human parathyroid
314	19	55.9	34	18	AAW17952	Human parathyroid
315	19	55.9	34	19	AAW67277	Parathyroid hormon
316	19	55.9	34	19	AAW67283	Parathyroid hormon
317	19	55.9	34	19	AAW67287	Parathyroid hormon
318	19	55.9	34	19	AAW48394	Human PTH/PTHrP hy
319	19	55.9	36	15	AAR58274	[Ala15]-hPTH(1-36)
320	19	55.9	36	15	AAR58231	[Ala31]-hPTH(1-36)
321	19	55.9	38	15	AAR58061	[Ile15]-hPTH(1-38)
322	19	55.9	38	15	AAR58167	[Ile31,Arg33]-hPTH
323	19	55.9	38	15	AAR58112	[Tyr15]-hPTH(1-38)
324	19	55.9	38	15	AAR58113	[Arg15]-hPTH(1-38)
325	19	55.9	38	15	AAR58114	[Val15]-hPTH(1-38)
326	18	52.9	28	13	AAR22058	Modified bovine PT
327	18	52.9	28	23	AAU73046	Parathyroid hormon
328	18	52.9	29	17	AAR88836	Human parathyroid
329	18	52.9	29	23	AAU73063	Parathyroid hormon
330	18	52.9	30	23	AAU73178	Parathyroid hormon
331	18	52.9	32	22	AAB91096	Parathyroid hormon
332	18	52.9	32	23	AAE23739	Bovine parathyroid
333	18	52.9	32	23	AAE18402	Bovine PTH peptide
334	18	52.9	32	23	AAU73042	Parathyroid hormon
335	18	52.9	34	11	AAR07918	Bovine parathyroid

336	18	52.9	34	11	AAR08299	Bovine parathyroid
337	18	52.9	34	14	AAR41551	[Thr16]hPTH (1-34)
338	18	52.9	34	14	AAR41552	[Glu16]hPTH (1-34)
339	18	52.9	34	14	AAR41553	[Lys16]hPTH (1-34)
340	18	52.9	34	14	AAR41571	[D-Lys16]hPTH (1-3
341	18	52.9	34	14	AAR41573	[Gln16]hPTH (1-34)
342	18	52.9	34	14	AAR41574	[Ser16]hPTH (1-34)
343	18	52.9	34	14	AAR41575	[Gly16]hPTH (1-34)
344	18	52.9	34	14	AAR41576	[Lys16]hPTH (1-34)
345	18	52.9	34	17	AAR99979	Bovine parathyroid
346	18	52.9	34	18	AAW08124	Human PTH derivati
347	18	52.9	34	18	AAW08111	Human PTH derivati
348	18	52.9	34	18	AAW19995	Cyclised bovine pa
349	18	52.9	34	18	AAW20001	Cyclised bovine pa
350	18	52.9	34	18	AAW20007	Cyclised bovine pa
351	18	52.9	34	18	AAW17953	Human parathyroid
352	18	52.9	34	18	AAW17963	Human PTH analogue
353	18	52.9	34	19	AAW61659	Parathyroid hormon
354	18	52.9	34	19	AAW65976	Bovine parathyroid
355	18	52.9	34	19	AAW42615	Bovine parathyroid
356	18	52.9	34	20	AAW81872	Bovine PTH N-termi
357	18	52.9	34	22	AAB84775	Parathyroid hormon
358	18	52.9	34	22	AAB96922	Parathyroid hormon
359	18	52.9	34	23	AAE23738	Bovine parathyroid
360	18	52.9	34	23	AAE18394	Bovine PTH peptide
361	18	52.9	34	23	AAU73034	Parathyroid hormon
362	18	52.9	36	15	AAR58275	[Ala16]-hPTH(1-36)
363	18	52.9	36	15	AAR58229	[Ala30]-hPTH(1-36)
364	18	52.9	37	22	AAB86230	Bovine parathyroid
365	18	52.9	37	22	AAB86233	Canine parathyroid
366	18	52.9	37	23	ABB82204	Bovine parathyroid
367	18	52.9	38	15	AAR58036	[Gln16]-hPTH(1-38)
368	18	52.9	38	15	AAR58115	[Lys16]-hPTH(1-38)
369	18	52.9	38	15	AAR58116	[Ser16]-hPTH(1-38)
370	18	52.9	38	15	AAR58117	[Leu16]-hPTH(1-38)
371	18	52.9	38	15	AAR58118	[Ala16]-hPTH(1-38)
372	18	52.9	38	15	AAR58119	[Gly16]-hPTH(1-38)
373	17	50.0	28	13	AAR22059	Modified [Tyr_34]b
374	17	50.0	28	13	AAR22060	Modified [D-Trp_12
375	17	50.0	28	17	AAR88837	Human parathyroid
376	17	50.0	28	21	AAV98048	Human parathyroid
377	17	50.0	28	21	AAV98050	Human parathyroid
378	17	50.0	28	21	AAV98052	Human parathyroid
379	17	50.0	28	22	AAB91115	Parathyroid hormon
380	17	50.0	28	23	AAE18405	Bovine PTH peptide
381	17	50.0	28	23	AAU73047	Parathyroid hormon
382	17	50.0	28	23	AAU73050	Parathyroid hormon
383	17	50.0	28	23	AAU73064	Parathyroid hormon
384	17	50.0	29	12	AAR11731	Adenine-rich PTH-(
385	17	50.0	29	23	AAU73179	Parathyroid hormon
386	17	50.0	31	5	AAP40510	Bovine parathyroid
387	17	50.0	31	21	AAV96973	Parathyroid hormon
388	17	50.0	31	21	AAV96974	Parathyroid hormon
389	17	50.0	34	11	AAR07921	Bovine parathyroid
390	17	50.0	34	11	AAR08302	Bovine parathyroid
391	17	50.0	34	14	AAR41577	[Lys16, Asp17]hPTH
392	17	50.0	34	14	AAR41578	[Lys14,15,16,17]hP

393	17	50.0	34	14	AAR41579	[Lys15,15,17]hPTH
394	17	50.0	34	14	AAR41580	[Lys16,17]hPTH (1-
395	17	50.0	34	14	AAR41581	[Arg16,17]hPTH (1-
396	17	50.0	34	14	AAR41582	[Arg15,16,17]hPTH
397	17	50.0	34	17	AAW14308	Cyclic parathyroid
398	17	50.0	34	17	AAW14309	Cyclic parathyroid
399	17	50.0	34	17	AAW14310	Cyclic parathyroid
400	17	50.0	34	17	AAW14311	Cyclic parathyroid
401	17	50.0	34	17	AAW14312	Cyclic parathyroid
402	17	50.0	34	17	AAW14313	Cyclic parathyroid
403	17	50.0	34	17	AAW14314	Cyclic parathyroid
404	17	50.0	34	17	AAW14315	Cyclic parathyroid
405	17	50.0	34	18	AAW08122	Human PTH derivati
406	17	50.0	34	18	AAW08123	Human PTH derivati
407	17	50.0	34	18	AAW17958	Human parathyroid
408	17	50.0	34	18	AAW01610	Parathyroid hormon
409	17	50.0	34	19	AAW67293	Parathyroid hormon
410	17	50.0	36	15	AAR58190	[Ala29]-hPTH(1-36)
411	17	50.0	36	15	AAR58212	[Ala17]-hPTH(1-36)
412	17	50.0	38	15	AAR58120	[Ala17]-hPTH(1-38)
413	17	50.0	38	15	AAR58121	[Met17]-hPTH(1-38)
414	17	50.0	38	15	AAR58122	[Ile17]-hPTH(1-38)
415	16	47.1	28	21	ABJ10775	Human parathyroid
416	16	47.1	34	13	AAR22291	Human parathyroid
417	16	47.1	34	13	AAR22295	Human parathyroid
418	16	47.1	34	15	AAR58239	Isopropyl-[Nle8,18
419	16	47.1	34	15	AAR58241	[Nle8,18,D-Asn33,D
420	16	47.1	34	17	AAW14316	Cyclic parathyroid
421	16	47.1	34	17	AAR99981	Porcine parathyroi
422	16	47.1	34	18	AAW17947	Human parathyroid
423	16	47.1	34	18	AAW17951	Human parathyroid
424	16	47.1	34	19	AAW67282	Parathyroid hormon
425	16	47.1	34	19	AAW67286	Parathyroid hormon
426	16	47.1	34	19	AAW67298	Parathyroid hormon
427	16	47.1	34	19	AAW61660	Parathyroid hormon
428	16	47.1	34	19	AAW65977	Porcine parathyroi
429	16	47.1	34	19	AAW42616	Porcine parathyroi
430	16	47.1	34	20	AAW92218	Analogue of parath
431	16	47.1	34	20	AAW92219	Analogue of parath
432	16	47.1	34	20	AAW03920	Analogue of parath
433	16	47.1	34	20	AAW03921	Analogue of parath
434	16	47.1	34	20	AAW03922	Analogue of parath
435	16	47.1	34	20	AAW03923	Analogue of parath
436	16	47.1	34	20	AAW03924	Analogue of parath
437	16	47.1	34	20	AAW03925	Analogue of parath
438	16	47.1	34	20	AAW03926	Analogue of parath
439	16	47.1	34	20	AAW03927	Analogue of parath
440	16	47.1	34	20	AAW03928	Analogue of parath
441	16	47.1	34	20	AAW03929	Analogue of parath
442	16	47.1	34	20	AAW03930	Analogue of parath
443	16	47.1	34	20	AAW03931	Analogue of parath
444	16	47.1	34	20	AAW03932	Analogue of parath
445	16	47.1	34	20	AAW03933	Analogue of parath
446	16	47.1	34	20	AAW92236	Analogue of parath
447	16	47.1	34	20	AAW92237	Analogue of parath
448	16	47.1	34	20	AAW92238	Analogue of parath
449	16	47.1	34	20	AAW92239	Analogue of parath

450	16	47.1	34	20	AAW92240	Analogue of parath
451	16	47.1	34	20	AAW92241	Analogue of parath
452	16	47.1	34	20	AAW92242	Analogue of parath
453	16	47.1	34	20	AAW92243	Analogue of parath
454	16	47.1	34	20	AAW92244	Analogue of parath
455	16	47.1	34	20	AAW92245	Analogue of parath
456	16	47.1	34	20	AAW92246	Analogue of parath
457	16	47.1	34	20	AAW92247	Analogue of parath
458	16	47.1	34	20	AAW92248	Analogue of parath
459	16	47.1	34	20	AAW92249	Analogue of parath
460	16	47.1	34	20	AAW92250	Analogue of parath
461	16	47.1	34	20	AAW92251	Analogue of parath
462	16	47.1	34	20	AAW92252	Analogue of parath
463	16	47.1	34	20	AAW92253	Analogue of parath
464	16	47.1	34	20	AAW92254	Analogue of parath
465	16	47.1	34	20	AAW92255	Analogue of parath
466	16	47.1	34	20	AAW92256	Analogue of parath
467	16	47.1	34	20	AAW92257	Analogue of parath
468	16	47.1	34	20	AAW92258	Analogue of parath
469	16	47.1	34	20	AAW92259	Analogue of parath
470	16	47.1	34	20	AAW92260	Analogue of parath
471	16	47.1	34	20	AAW92261	Analogue of parath
472	16	47.1	34	20	AAW92262	Analogue of parath
473	16	47.1	34	20	AAW92263	Analogue of parath
474	16	47.1	34	20	AAW92264	Analogue of parath
475	16	47.1	34	20	AAW92265	Analogue of parath
476	16	47.1	34	20	AAW92266	Analogue of parath
477	16	47.1	34	20	AAW92267	Analogue of parath
478	16	47.1	34	20	AAW92268	Analogue of parath
479	16	47.1	34	20	AAW92269	Analogue of parath
480	16	47.1	34	20	AAW92270	Analogue of parath
481	16	47.1	34	20	AAW92271	Analogue of parath
482	16	47.1	34	20	AAW92272	Analogue of parath
483	16	47.1	34	20	AAW92273	Analogue of parath
484	16	47.1	34	20	AAW92274	Analogue of parath
485	16	47.1	34	20	AAW92275	Analogue of parath
486	16	47.1	34	20	AAW92276	Analogue of parath
487	16	47.1	34	20	AAW92277	Analogue of parath
488	16	47.1	34	20	AAW92278	Analogue of parath
489	16	47.1	34	20	AAW92279	Analogue of parath
490	16	47.1	34	20	AAW92280	Analogue of parath
491	16	47.1	34	20	AAW92281	Analogue of parath
492	16	47.1	34	20	AAW92282	Analogue of parath
493	16	47.1	34	20	AAW92283	Analogue of parath
494	16	47.1	34	20	AAW92284	Analogue of parath
495	16	47.1	34	20	AAW92285	Analogue of parath
496	16	47.1	34	20	AAW92286	Analogue of parath
497	16	47.1	34	20	AAW92287	Analogue of parath
498	16	47.1	34	20	AAW92288	Analogue of parath
499	16	47.1	34	20	AAW92289	Analogue of parath
500	16	47.1	34	20	AAW92290	Analogue of parath
501	16	47.1	34	20	AAW92291	Analogue of parath
502	16	47.1	34	20	AAW92292	Analogue of parath
503	16	47.1	34	20	AAW92293	Analogue of parath
504	16	47.1	34	20	AAW92294	Analogue of parath
505	16	47.1	34	20	AAW92295	Analogue of parath
506	16	47.1	34	20	AAW92296	Analogue of parath

507	16	47.1	34	20	AAV03946	Analogue of parath
508	16	47.1	34	20	AAV03949	Analogue of parath
509	16	47.1	34	20	AAV03950	Analogue of parath
510	16	47.1	34	20	AAV03951	Analogue of parath
511	16	47.1	34	20	AAV03952	Analogue of parath
512	16	47.1	34	20	AAV03953	Analogue of parath
513	16	47.1	34	20	AAV03954	Analogue of parath
514	16	47.1	34	20	AAV03955	Analogue of parath
515	16	47.1	34	20	AAV03956	Analogue of parath
516	16	47.1	34	20	AAW92198	Analogue of parath
517	16	47.1	34	20	AAW92199	Analogue of parath
518	16	47.1	34	20	AAW92200	Analogue of parath
519	16	47.1	34	20	AAW92201	Analogue of parath
520	16	47.1	34	20	AAW92202	Analogue of parath
521	16	47.1	34	20	AAW92183	Analogue of parath
522	16	47.1	34	20	AAW92184	Analogue of parath
523	16	47.1	34	20	AAW92185	Analogue of parath
524	16	47.1	34	20	AAW92186	Analogue of parath
525	16	47.1	34	20	AAW92187	Analogue of parath
526	16	47.1	34	20	AAW92167	Analogue of parath
527	16	47.1	34	20	AAW92188	Analogue of parath
528	16	47.1	34	20	AAW92189	Analogue of parath
529	16	47.1	34	20	AAW92190	Analogue of parath
530	16	47.1	34	20	AAW92191	Analogue of parath
531	16	47.1	34	20	AAW92192	Analogue of parath
532	16	47.1	34	20	AAW92193	Analogue of parath
533	16	47.1	34	20	AAW92194	Analogue of parath
534	16	47.1	34	20	AAW92195	Analogue of parath
535	16	47.1	34	20	AAW92196	Analogue of parath
536	16	47.1	34	20	AAW92197	Analogue of parath
537	16	47.1	34	20	AAW92166	Analogue of parath
538	16	47.1	34	20	AAW92168	Analogue of parath
539	16	47.1	34	20	AAW92169	Analogue of parath
540	16	47.1	34	20	AAW92170	Analogue of parath
541	16	47.1	34	20	AAW92171	Analogue of parath
542	16	47.1	34	20	AAW92172	Analogue of parath
543	16	47.1	34	20	AAW92173	Analogue of parath
544	16	47.1	34	20	AAW92174	Analogue of parath
545	16	47.1	34	20	AAW92175	Analogue of parath
546	16	47.1	34	20	AAW92176	Analogue of parath
547	16	47.1	34	20	AAW92177	Analogue of parath
548	16	47.1	34	20	AAW92178	Analogue of parath
549	16	47.1	34	20	AAW92179	Analogue of parath
550	16	47.1	34	20	AAW92180	Analogue of parath
551	16	47.1	34	20	AAW92181	Analogue of parath
552	16	47.1	34	20	AAW92182	Analogue of parath
553	16	47.1	34	20	AAW92152	Analogue of parath
554	16	47.1	34	20	AAW92150	Analogue of parath
555	16	47.1	34	20	AAW92151	Analogue of parath
556	16	47.1	34	20	AAW92153	Analogue of parath
557	16	47.1	34	20	AAW92154	Analogue of parath
558	16	47.1	34	20	AAW92155	Analogue of parath
559	16	47.1	34	20	AAW92156	Analogue of parath
560	16	47.1	34	20	AAW92157	Analogue of parath
561	16	47.1	34	20	AAW92158	Analogue of parath
562	16	47.1	34	20	AAW92159	Analogue of parath
563	16	47.1	34	20	AAW92160	Analogue of parath

564	16	47.1	34	20	AAW92161	Analogue of parath
565	16	47.1	34	20	AAW92162	Analogue of parath
566	16	47.1	34	20	AAW92163	Analogue of parath
567	16	47.1	34	20	AAW92164	Analogue of parath
568	16	47.1	34	20	AAW92165	Analogue of parath
569	16	47.1	34	20	AAW92148	Analogue of parath
570	16	47.1	34	20	AAW92149	Analogue of parath
571	16	47.1	34	20	AAW81873	Porcine PTH N-term
572	16	47.1	34	21	ABJ10735	Human parathyroid
573	16	47.1	34	21	ABJ10739	Human parathyroid
574	16	47.1	34	21	ABJ10740	Human parathyroid
575	16	47.1	34	21	ABJ10742	Human parathyroid
576	16	47.1	34	21	ABJ10743	Human parathyroid
577	16	47.1	34	22	AAB91084	Parathyroid hormon
578	16	47.1	34	22	AAB91085	Parathyroid hormon
579	16	47.1	34	22	AAB91087	Parathyroid hormon
580	16	47.1	34	23	AAU73036	Parathyroid hormon
581	16	47.1	35	2	AAP10140	h-PTH antigen. Sy
582	16	47.1	36	15	AAR58277	[Nle18]-hPTH(1-36)
583	16	47.1	36	15	AAR58183	[Gln18]-hPTH(1-36)
584	16	47.1	36	15	AAR58184	[Tyr18]-hPTH(1-36)
585	16	47.1	36	15	AAR58042	[L8,D10,K11,L18]-h
586	16	47.1	36	15	AAR58044	[L8,D10,K11,A17,L1
587	16	47.1	36	15	AAR58055	[L8,Q18]-hPTH(1-36
588	16	47.1	36	15	AAR58057	[L8,D10,A16,Q18]-h
589	16	47.1	36	15	AAR58071	[Aib3, Gln18]-hPTH
590	16	47.1	36	15	AAR55820	[L8,D10,K11,Q18]-h
591	16	47.1	36	15	AAR55824	[L8,D10,K11,A16,Q1
592	16	47.1	36	15	AAR58027	[A1,A3,L8,Q18]-hPT
593	16	47.1	36	15	AAR58031	[L8,K11,Q18]-hPTH(
594	16	47.1	36	15	AAR58072	Isopropyl-[L8,D10,
595	16	47.1	36	15	AAR58074	[L8,Y18]-hPTH(1-36
596	16	47.1	36	15	AAR58088	[1-amino-cyclopent
597	16	47.1	37	22	AAB86232	Porcine parathyroi
598	16	47.1	38	15	AAR58159	[Val28]-hPTH(1-38)
599	16	47.1	38	15	AAR58160	[Ile28]-hPTH(1-38)
600	15	44.1	28	13	AAR22061	Modified [Nle_8,18
601	15	44.1	28	13	AAR22062	Modified [Nle_8,18
602	15	44.1	28	13	AAR22067	Modified [Nle_8,_1
603	15	44.1	28	13	AAR22068	Modified [Nle_8,_1
604	15	44.1	28	17	AAR88838	Human parathyroid
605	15	44.1	28	21	ABJ10774	Human parathyroid
606	15	44.1	28	22	AAB81074	Human parathyroid
607	15	44.1	28	23	AAE18404	Bovine PTH peptide
608	15	44.1	28	23	AAU73045	Parathyroid hormon
609	15	44.1	28	23	AAU73048	Parathyroid hormon
610	15	44.1	28	23	AAU73049	Parathyroid hormon
611	15	44.1	29	17	AAR88839	Human parathyroid
612	15	44.1	29	22	AAB81075	Human parathyroid
613	15	44.1	30	17	AAR88833	Human parathyroid
614	15	44.1	30	19	AAW42052	Human parathyroid
615	15	44.1	30	22	AAB91089	Parathyroid hormon
616	15	44.1	30	22	AAB91092	Parathyroid hormon
617	15	44.1	30	23	AAU73062	Parathyroid hormon
618	15	44.1	31	5	AAP40511	Bovine parathyroid
619	15	44.1	31	5	AAP40761	Human parathyroid
620	15	44.1	31	17	AAR88831	Human parathyroid

621	15	44.1	31	19	AAW42056	Human parathyroid
622	15	44.1	31	19	AAW42057	Human parathyroid
623	15	44.1	31	19	AAW42060	Human parathyroid
624	15	44.1	31	19	AAW42062	Human parathyroid
625	15	44.1	31	19	AAW42067	Human parathyroid
626	15	44.1	31	19	AAW42049	Human parathyroid
627	15	44.1	31	19	AAW42050	Human parathyroid
628	15	44.1	31	19	AAW42053	Human parathyroid
629	15	44.1	31	21	AAU96975	Parathyroid hormon
630	15	44.1	31	23	AAU73040	Parathyroid hormon
631	15	44.1	31	23	AAU82640	Analogue of human
632	15	44.1	32	22	AAB91088	Parathyroid hormon
633	15	44.1	32	22	AAB91090	Parathyroid hormon
634	15	44.1	32	22	AAB91091	Parathyroid hormon
635	15	44.1	32	23	AAE18403	Bovine PTH peptide
636	15	44.1	32	23	AAU73041	Parathyroid hormon
637	15	44.1	32	23	AAU73043	Parathyroid hormon
638	15	44.1	34	6	AAP50517	Sequence of methio
639	15	44.1	34	11	AAR07924	Bovine parathyroid
640	15	44.1	34	11	AAR07925	Human parathyroid
641	15	44.1	34	11	AAR08305	Bovine parathyroid
642	15	44.1	34	11	AAR08306	Human parathyroid
643	15	44.1	34	13	AAR22298	Human parathyroid
644	15	44.1	34	13	AAR22299	Human parathyroid
645	15	44.1	34	14	AAR41554	[Thr27]hPTH (1-34)
646	15	44.1	34	14	AAR41555	[Asn27]hPTH (1-34)
647	15	44.1	34	14	AAR41558	[Ser27]hPTH (1-34)
648	15	44.1	34	14	AAR41559	[Gly27]hPTH (1-34)
649	15	44.1	34	14	AAR41560	[His27]hPTH (1-34)
650	15	44.1	34	15	AAR45528	Parathyroid hormon
651	15	44.1	34	16	AAR69055	PTH analogue with
652	15	44.1	34	17	AAR88829	Human parathyroid
653	15	44.1	34	17	AAR88834	Human parathyroid
654	15	44.1	34	18	AAW13352	Truncated parathyr
655	15	44.1	34	18	AAW12651	Parathyroid hormon
656	15	44.1	34	18	AAW08130	Human PTH derivati
657	15	44.1	34	18	AAW20004	Cyclised [Nle 8,18
658	15	44.1	34	18	AAW19997	Cyclised [Nle 8,18
659	15	44.1	34	18	AAW19998	Cyclised [Nle 8,18
660	15	44.1	34	18	AAW20003	Cyclised [Nle 8,18
661	15	44.1	34	18	AAW20009	Cyclised [Nle 8,18
662	15	44.1	34	18	AAW20010	Cyclised [Nle 8,18
663	15	44.1	34	18	AAW17940	Human PTH analogue
664	15	44.1	34	18	AAW17969	Human parathyroid
665	15	44.1	34	18	AAW17970	Human PTH analogue
666	15	44.1	34	18	AAW17964	Human PTH analogue
667	15	44.1	34	18	AAW17954	Human parathyroid
668	15	44.1	34	18	AAW17956	Human parathyroid
669	15	44.1	34	18	AAW17962	Human PTH analogue
670	15	44.1	34	19	AAW67275	Parathyroid hormon
671	15	44.1	34	19	AAW67292	Parathyroid hormon
672	15	44.1	34	19	AAW67297	Parathyroid hormon
673	15	44.1	34	19	AAW61725	Parathyroid hormon
674	15	44.1	34	19	AAW66053	Parathyroid hormon
675	15	44.1	34	19	AAW42602	Parathyroid hormon
676	15	44.1	34	19	AAW42054	Human parathyroid
677	15	44.1	34	19	AAW42055	Human parathyroid

678	15	44.1	34	19	AAW48395	Human PTH/PTHrP hy
679	15	44.1	34	20	AAW74396	Modified parathyro
680	15	44.1	34	20	AAW81945	Synthetic PTH and
681	15	44.1	34	21	ABJ10705	Human parathyroid
682	15	44.1	34	21	ABJ10707	Human parathyroid
683	15	44.1	34	21	ABJ10708	Human parathyroid
684	15	44.1	34	21	ABJ10709	Human parathyroid
685	15	44.1	34	21	ABJ10710	Human parathyroid
686	15	44.1	34	21	ABJ10711	Human parathyroid
687	15	44.1	34	21	ABJ10715	Human parathyroid
688	15	44.1	34	21	ABJ10716	Human parathyroid
689	15	44.1	34	21	ABJ10718	Human parathyroid
690	15	44.1	34	21	ABJ10720	Human parathyroid
691	15	44.1	34	21	ABJ10721	Human parathyroid
692	15	44.1	34	21	ABJ10723	Human parathyroid
693	15	44.1	34	21	ABJ10725	Human parathyroid
694	15	44.1	34	21	ABJ10726	Human parathyroid
695	15	44.1	34	21	ABJ10728	Human parathyroid
696	15	44.1	34	21	ABJ10731	Human parathyroid
697	15	44.1	34	21	ABJ10732	Human parathyroid
698	15	44.1	34	21	ABJ10734	Human parathyroid
699	15	44.1	34	21	ABJ10738	Human parathyroid
700	15	44.1	34	21	ABJ10741	Human parathyroid
701	15	44.1	34	21	ABJ10744	Human parathyroid
702	15	44.1	34	21	ABJ10745	Human parathyroid
703	15	44.1	34	21	ABJ10746	Human parathyroid
704	15	44.1	34	21	ABJ10747	Human parathyroid
705	15	44.1	34	21	ABJ10748	Human parathyroid
706	15	44.1	34	21	ABJ10749	Human parathyroid
707	15	44.1	34	21	ABJ10750	Human parathyroid
708	15	44.1	34	21	ABJ10751	Human parathyroid
709	15	44.1	34	21	ABJ10752	Human parathyroid
710	15	44.1	34	21	ABJ10753	Human parathyroid
711	15	44.1	34	21	ABJ10754	Human parathyroid
712	15	44.1	34	21	ABJ10755	Human parathyroid
713	15	44.1	34	21	ABJ10756	Human parathyroid
714	15	44.1	34	21	ABJ10761	Human parathyroid
715	15	44.1	34	21	ABJ10762	Human parathyroid
716	15	44.1	34	21	ABJ10763	Human parathyroid
717	15	44.1	34	21	ABJ10764	Human parathyroid
718	15	44.1	34	21	ABJ10765	Human parathyroid
719	15	44.1	34	21	ABJ10766	Human parathyroid
720	15	44.1	34	21	ABJ10767	Human parathyroid
721	15	44.1	34	21	ABJ10768	Human parathyroid
722	15	44.1	34	21	ABJ10770	Human parathyroid
723	15	44.1	34	21	ABJ10771	Human parathyroid
724	15	44.1	34	21	ABJ10777	Human parathyroid
725	15	44.1	34	23	AAE18396	Bovine PTH peptide
726	15	44.1	34	23	AAE18397	Human PTH peptide
727	15	44.1	34	23	AAU73031	Parathyroid hormon
728	15	44.1	34	23	AAU73033	Parathyroid hormon
729	15	44.1	34	23	AAU73035	Parathyroid hormon
730	15	44.1	35	16	AAR74518	Parathyroid hormon
731	15	44.1	35	16	AAR74519	Parathyroid hormon
732	15	44.1	35	16	AAR74520	Parathyroid hormon
733	15	44.1	35	16	AAR74527	Human parathyroid
734	15	44.1	35	16	AAR74464	Parathyroid hormon

735	15	44.1	35	16	AAR74465	Parathyroid hormon
736	15	44.1	35	16	AAR74466	Parathyroid hormon
737	15	44.1	35	16	AAR74467	Parathyroid hormon
738	15	44.1	35	16	AAR74468	Parathyroid hormon
739	15	44.1	35	16	AAR74469	Parathyroid hormon
740	15	44.1	35	16	AAR74470	Parathyroid hormon
741	15	44.1	35	16	AAR74471	Parathyroid hormon
742	15	44.1	35	16	AAR74472	Parathyroid hormon
743	15	44.1	35	16	AAR74473	Parathyroid hormon
744	15	44.1	35	16	AAR74474	Parathyroid hormon
745	15	44.1	35	16	AAR74475	Parathyroid hormon
746	15	44.1	35	16	AAR74476	Parathyroid hormon
747	15	44.1	35	16	AAR74477	Parathyroid hormon
748	15	44.1	35	16	AAR74478	Parathyroid hormon
749	15	44.1	35	16	AAR74479	Parathyroid hormon
750	15	44.1	35	16	AAR74448	Parathyroid hormon
751	15	44.1	35	16	AAR74449	Parathyroid hormon
752	15	44.1	35	16	AAR74450	Parathyroid hormon
753	15	44.1	35	16	AAR74451	Parathyroid hormon
754	15	44.1	35	16	AAR74452	Parathyroid hormon
755	15	44.1	35	16	AAR74453	Parathyroid hormon
756	15	44.1	35	16	AAR74454	Parathyroid hormon
757	15	44.1	35	16	AAR74455	Parathyroid hormon
758	15	44.1	35	16	AAR74456	Parathyroid hormon
759	15	44.1	35	16	AAR74457	Parathyroid hormon
760	15	44.1	35	16	AAR74458	Parathyroid hormon
761	15	44.1	35	16	AAR74459	Parathyroid hormon
762	15	44.1	35	16	AAR74460	Parathyroid hormon
763	15	44.1	35	16	AAR74461	Parathyroid hormon
764	15	44.1	35	16	AAR74462	Parathyroid hormon
765	15	44.1	35	16	AAR74463	Parathyroid hormon
766	15	44.1	35	16	AAR74432	Parathyroid hormon
767	15	44.1	35	16	AAR74433	Parathyroid hormon
768	15	44.1	35	16	AAR74434	Parathyroid hormon
769	15	44.1	35	16	AAR74435	Parathyroid hormon
770	15	44.1	35	16	AAR74436	Parathyroid hormon
771	15	44.1	35	16	AAR74437	Parathyroid hormon
772	15	44.1	35	16	AAR74438	Parathyroid hormon
773	15	44.1	35	16	AAR74439	Parathyroid hormon
774	15	44.1	35	16	AAR74440	Parathyroid hormon
775	15	44.1	35	16	AAR74441	Parathyroid hormon
776	15	44.1	35	16	AAR74442	Parathyroid hormon
777	15	44.1	35	16	AAR74443	Parathyroid hormon
778	15	44.1	35	16	AAR74444	Parathyroid hormon
779	15	44.1	35	16	AAR74445	Parathyroid hormon
780	15	44.1	35	16	AAR74446	Parathyroid hormon
781	15	44.1	35	16	AAR74447	Parathyroid hormon
782	15	44.1	35	16	AAR74429	Parathyroid hormon
783	15	44.1	35	16	AAR74430	Parathyroid hormon
784	15	44.1	35	16	AAR74431	Parathyroid hormon
785	15	44.1	35	16	AAR74398	Parathyroid hormon
786	15	44.1	35	16	AAR74399	Parathyroid hormon
787	15	44.1	35	16	AAR74400	Parathyroid hormon
788	15	44.1	35	16	AAR74394	Parathyroid hormon
789	15	44.1	35	16	AAR74395	Parathyroid hormon
790	15	44.1	35	16	AAR74396	Parathyroid hormon
791	15	44.1	35	16	AAR74397	Parathyroid hormon

792	15	44.1	35	23	AAU73175	Parathyroid hormon
793	15	44.1	36	15	AAR58222	[His27]-hPTH(1-36)
794	15	44.1	36	15	AAR58223	[Phe27]-hPTH(1-36)
795	15	44.1	36	15	AAR58224	[Nle27]-hPTH(1-36)
796	15	44.1	36	15	AAR58225	[Asn27]-hPTH(1-36)
797	15	44.1	36	15	AAR58226	[Ala27]-hPTH(1-36)
798	15	44.1	36	15	AAR58214	[Ala19]-hPTH(1-36)
799	15	44.1	36	15	AAR58041	[L8,D10,K11,S14,I1
800	15	44.1	36	15	AAR58043	[L8,Q16,D17,L18,R1
801	15	44.1	36	15	AAR58046	[L8,A16,D17,L18,A1
802	15	44.1	36	15	AAR58047	[L8,D10,A16,D17,L1
803	15	44.1	36	15	AAR58050	[L8,A16,D17,Q18,A1
804	15	44.1	36	15	AAR58051	[L8,A16,A17,Q18,A1
805	15	44.1	36	15	AAR58052	[L8,A17,Q18,A19]-h
806	15	44.1	36	15	AAR58067	[L8,A16,A17,A18,A1
807	15	44.1	36	15	AAR58069	Isopropyl-[L8,K(Is
808	15	44.1	36	15	AAR58070	Isopropyl-[L8,K(Is
809	15	44.1	36	15	AAR55822	[L8,D10,K11,A16,Q1
810	15	44.1	36	15	AAR55825	[L8,A16,Q18,A19]-h
811	15	44.1	36	15	AAR58086	[1-amino-cyclopent
812	15	44.1	38	15	AAR58136	[Arg19]-hPTH(1-38)
813	15	44.1	38	15	AAR58154	[Val27]-hPTH(1-38)
814	15	44.1	38	15	AAR58155	[Ile27]-hPTH(1-38)
815	15	44.1	38	15	AAR58156	[Leu27]-hPTH(1-38)
816	15	44.1	38	15	AAR58157	[Arg27]-hPTH(1-38)
817	15	44.1	38	15	AAR58158	[Ala27]-hPTH(1-38)
818	15	44.1	38	15	AAR58123	[Ser19]-hPTH(1-38)
819	15	44.1	38	15	AAR58124	[Lys19]-hPTH(1-38)
820	15	44.1	38	15	AAR58125	[Leu19]-hPTH(1-38)
821	15	44.1	38	15	AAR58126	[Ala19]-hPTH(1-38)
822	15	44.1	38	15	AAR58127	[Tyr19]-hPTH(1-38)
823	15	44.1	38	15	AAR58128	[Met19]-hPTH(1-38)
824	15	44.1	38	15	AAR58129	[His19]-hPTH(1-38)
825	15	44.1	38	15	AAR58130	[Val19]-hPTH(1-38)
826	15	44.1	38	15	AAR58131	[Gly19]-hPTH(1-38)
827	15	44.1	38	15	AAR58132	[Pro19]-hPTH(1-38)
828	15	44.1	38	15	AAR58133	[Asp19]-hPTH(1-38)
829	15	44.1	38	15	AAR58134	[Ile19]-hPTH(1-38)
830	14	41.2	28	23	AAU73066	Parathyroid hormon
831	14	41.2	30	23	AAU73057	Parathyroid hormon
832	14	41.2	33	17	AAW15814	[Leu(8),Trp(10),Al
833	14	41.2	34	14	AAR41556	[Gln26,27]hPTH(1-
834	14	41.2	34	14	AAR41566	[Arg 26,27]hPTH(1
835	14	41.2	34	14	AAR41567	[Gln26]hPTH(1-34)
836	14	41.2	34	15	AAR55817	[L8,Q18,T33,A34]-h
837	14	41.2	34	15	AAR55819	[L8,A16,Q18,T33,A3
838	14	41.2	34	15	AAR55821	[L8,D10,K11,Q18,T3
839	14	41.2	34	15	AAR55823	[L8,D10,K11,A16,Q1
840	14	41.2	34	15	AAR58021	[L8,D10,A16,Q18,T3
841	14	41.2	34	15	AAR58034	Isopropyl-[L8,K(Is
842	14	41.2	34	17	AAW15813	[Leu(8),Trp(10),Al
843	14	41.2	34	17	AAW15815	[Leu(8),Trp(10),DL
844	14	41.2	34	17	AAW15828	N-alpha-acylated [
845	14	41.2	34	18	AAW08132	Human PTH derivati
846	14	41.2	34	18	AAW17960	Human PTH analogue
847	14	41.2	34	20	AAV02587	Parathyroid hormon
848	14	41.2	34	21	ABJ10757	Human parathyroid

849	14	41.2	35	16	AAR74515	Parathyroid hormon
850	14	41.2	35	16	AAR74516	Parathyroid hormon
851	14	41.2	35	16	AAR74517	Parathyroid hormon
852	14	41.2	35	16	AAR74480	Parathyroid hormon
853	14	41.2	35	16	AAR74401	Parathyroid hormon
854	14	41.2	35	16	AAR74409	Parathyroid hormon
855	14	41.2	35	16	AAR74412	Parathyroid hormon
856	14	41.2	36	15	AAR58290	[Ala26] -hPTH(1-36)
857	14	41.2	36	15	AAR58279	[Lys20] -hPTH(1-36)
858	14	41.2	36	15	AAR58218	[Gln26] -hPTH(1-36)
859	14	41.2	36	15	AAR58219	[Nle26] -hPTH(1-36)
860	14	41.2	38	15	AAR58137	[Phe20] -hPTH(1-38)
861	14	41.2	38	15	AAR58153	[Arg26] -hPTH(1-38)
862	13	38.2	32	22	AAB84835	Parathyroid hormon
863	13	38.2	32	22	AAB96906	Parathyroid hormon
864	13	38.2	34	13	AAR22297	Human parathyroid
865	13	38.2	34	14	AAR34456	Human parathyroid
866	13	38.2	34	14	AAR34457	Human parathyroid
867	13	38.2	34	14	AAR41557	[Gln25,26,27]hPTH
868	13	38.2	34	15	AAR58195	[S14,I15,Q16,D17,L
869	13	38.2	34	15	AAR58045	[L8,Q16,D17,L18,R1
870	13	38.2	34	15	AAR58049	[L8,D10,K11,Q16,D1
871	13	38.2	34	15	AAR58056	[L8,D10,K11,A16,Q1
872	13	38.2	34	15	AAR58058	[L8,D10,K11,A16,Q1
873	13	38.2	34	15	AAR55818	[L8,A16,Q18,A19,T3
874	13	38.2	34	18	AAW08131	Human PTH derivati
875	13	38.2	34	21	ABJ10758	Human parathyroid
876	13	38.2	34	22	AAB84828	Parathyroid hormon
877	13	38.2	34	22	AAB96921	Parathyroid hormon
878	13	38.2	35	16	AAR74512	Parathyroid hormon
879	13	38.2	35	16	AAR74513	Parathyroid hormon
880	13	38.2	35	16	AAR74514	Parathyroid hormon
881	13	38.2	35	16	AAR74511	Parathyroid hormon
882	13	38.2	35	16	AAR74481	Parathyroid hormon
883	13	38.2	35	16	AAR74482	Parathyroid hormon
884	13	38.2	35	16	AAR74483	Parathyroid hormon
885	13	38.2	35	16	AAR74408	Parathyroid hormon
886	13	38.2	36	15	AAR58287	[Phe25] -hPTH(1-36)
887	13	38.2	36	15	AAR58288	[Lys25] -hPTH(1-36)
888	13	38.2	36	15	AAR58289	[Ala25] -hPTH(1-36)
889	13	38.2	36	15	AAR58192	[Gln25] -hPTH(1-36)
890	13	38.2	36	15	AAR58216	[Ala21] -hPTH(1-36)
891	13	38.2	38	15	AAR58138	[Ala21] -hPTH(1-38)
892	13	38.2	38	15	AAR58139	[Gly21] -hPTH(1-38)
893	13	38.2	38	15	AAR58140	[Phe21] -hPTH(1-38)
894	13	38.2	38	15	AAR58141	[Leu21] -hPTH(1-38)
895	13	38.2	38	15	AAR58142	[Asn21] -hPTH(1-38)
896	13	38.2	38	15	AAR58143	[Gln21] -hPTH(1-38)
897	13	38.2	38	15	AAR58144	[Ser21] -hPTH(1-38)
898	12	35.3	28	23	AAU73065	Parathyroid hormon
899	12	35.3	28	23	AAU73067	Parathyroid hormon
900	12	35.3	29	13	AAR22070	Modified rPTH(7-34
901	12	35.3	30	23	AAU73056	Parathyroid hormon
902	12	35.3	30	23	AAU73058	Parathyroid hormon
903	12	35.3	30	23	AAU73059	Parathyroid hormon
904	12	35.3	34	11	AAR07917	Rat parathyroid ho
905	12	35.3	34	11	AAR08298	Rat parathyroid ho

906	12	35.3	34	16	AAR62432	Accelerator peptid
907	12	35.3	34	17	AAR99980	Rat parathyroid ho
908	12	35.3	34	18	AAW19996	Cyclised rat parat
909	12	35.3	34	18	AAW20002	Cyclised rat parat
910	12	35.3	34	18	AAW20008	Cyclised rat parat
911	12	35.3	34	18	AAW17949	Human parathyroid
912	12	35.3	34	18	AAW17945	Human parathyroid
913	12	35.3	34	18	AAW17950	Human PTH analogue
914	12	35.3	34	19	AAW67280	Parathyroid hormon
915	12	35.3	34	19	AAW67284	Parathyroid hormon
916	12	35.3	34	19	AAW67285	Parathyroid hormon
917	12	35.3	34	19	AAW67288	Parathyroid hormon
918	12	35.3	34	19	AAW67289	Parathyroid hormon
919	12	35.3	34	19	AAW67294	Parathyroid hormon
920	12	35.3	34	19	AAW67295	Parathyroid hormon
921	12	35.3	34	19	AAW67296	Parathyroid hormon
922	12	35.3	34	19	AAW67303	Parathyroid hormon
923	12	35.3	34	19	AAW67304	Parathyroid hormon
924	12	35.3	34	19	AAW48396	Human PTH/PTHrP hy
925	12	35.3	34	21	ABJ10759	Human parathyroid
926	12	35.3	34	22	AAB84777	Native human parat
927	12	35.3	34	22	AAB96897	Rat parathyroid ho
928	12	35.3	34	22	AAB91100	Parathyroid hormon
929	12	35.3	34	23	AAU73037	Parathyroid hormon
930	12	35.3	34	24	ABP71499	Rat parathyroid ho
931	12	35.3	35	16	AAR74507	Parathyroid hormon
932	12	35.3	35	16	AAR74508	Parathyroid hormon
933	12	35.3	35	16	AAR74509	Parathyroid hormon
934	12	35.3	35	16	AAR74510	Parathyroid hormon
935	12	35.3	35	16	AAR74484	Parathyroid hormon
936	12	35.3	35	16	AAR74485	Parathyroid hormon
937	12	35.3	35	16	AAR74486	Parathyroid hormon
938	12	35.3	36	15	AAR58208	[A13,Q26,F27,D-F34
939	12	35.3	36	15	AAR58217	[Ala22]-hPTH(1-36)
940	12	35.3	36	15	AAR58053	[L8,A17,Q18,A19,R2
941	12	35.3	36	15	AAR58060	[L8,A16,Q18,A19,R2
942	12	35.3	36	15	AAR58064	[L8,S13,A16,Q18,A1
943	12	35.3	36	15	AAR58032	[L8,A16,D17,L18,R1
944	12	35.3	36	15	AAR58073	Isopropyl-[L8,S13,
945	12	35.3	37	22	AAB86231	Rat parathyroid ho
946	12	35.3	38	15	AAR58145	[Gly22]-hPTH(1-38)
947	12	35.3	38	15	AAR58146	[Leu22]-hPTH(1-38)
948	12	35.3	38	15	AAR58147	[His22]-hPTH(1-38)
949	12	35.3	38	15	AAR58148	[Ala22]-hPTH(1-38)
950	12	35.3	38	15	AAR58149	[Ile22]-hPTH(1-38)
951	12	35.3	38	15	AAR58150	[Val22]-hPTH(1-38)
952	12	35.3	38	15	AAR58151	[Ser22]-hPTH(1-38)
953	12	35.3	38	15	AAR58152	[Arg22]-hPTH(1-38)
954	11	32.4	28	9	AAP82184	Sequence of parath
955	11	32.4	28	13	AAR22071	Modified [Tyr_34]r
956	11	32.4	28	13	AAR22072	Modified [D-Trp_12
957	11	32.4	28	13	AAR22073	Modified [Nle_8,_1
958	11	32.4	28	13	AAR22074	Modified [Nle_8,_1
959	11	32.4	28	23	AAU73105	Parathyroid hormon
960	11	32.4	28	23	AAU73106	Parathyroid hormon
961	11	32.4	30	22	AAB84834	Parathyroid hormon
962	11	32.4	30	22	AAB96905	Parathyroid hormon

963	11	32.4	30	23	AAU73054	Parathyroid hormon
964	11	32.4	30	23	AAU73136	Parathyroid hormon
965	11	32.4	30	23	AAU73137	Parathyroid hormon
966	11	32.4	32	22	AAB91094	Parathyroid hormon
967	11	32.4	33	9	AAP82176	Sequence of parath
968	11	32.4	34	7	AAP61414	Peptide with parat
969	11	32.4	34	8	AAP71281	Parathyroid hormon
970	11	32.4	34	11	AAR07920	Rat parathyroid ho
971	11	32.4	34	11	AAR07923	Rat parathyroid ho
972	11	32.4	34	11	AAR08301	Rat parathyroid ho
973	11	32.4	34	11	AAR08304	Rat parathyroid ho
974	11	32.4	34	14	AAR34358	Human parathyroid
975	11	32.4	34	14	AAR34337	Bovine parathyroid
976	11	32.4	34	14	AAR34338	Bovine parathyroid
977	11	32.4	34	14	AAR34339	Bovine parathyroid
978	11	32.4	34	14	AAR34340	Bovine parathyroid
979	11	32.4	34	14	AAR34341	Bovine parathyroid
980	11	32.4	34	14	AAR34342	Bovine parathyroid
981	11	32.4	34	14	AAR34343	Bovine parathyroid
982	11	32.4	34	14	AAR34344	Bovine parathyroid
983	11	32.4	34	14	AAR34345	Bovine parathyroid
984	11	32.4	34	14	AAR34346	Bovine parathyroid
985	11	32.4	34	14	AAR34347	Bovine parathyroid
986	11	32.4	34	14	AAR34348	Bovine parathyroid
987	11	32.4	34	14	AAR34349	Bovine parathyroid
988	11	32.4	34	14	AAR34350	Bovine parathyroid
989	11	32.4	34	14	AAR34351	Bovine parathyroid
990	11	32.4	34	14	AAR34352	Bovine parathyroid
991	11	32.4	34	14	AAR34353	Human parathyroid
992	11	32.4	34	14	AAR34354	Human parathyroid
993	11	32.4	34	14	AAR34355	Human parathyroid
994	11	32.4	34	14	AAR34356	Human parathyroid
995	11	32.4	34	14	AAR34357	Human parathyroid
996	11	32.4	34	14	AAR34359	Human parathyroid
997	11	32.4	34	14	AAR34360	Human parathyroid
998	11	32.4	34	14	AAR34361	Human parathyroid
999	11	32.4	34	14	AAR34362	Human parathyroid
1000	11	32.4	34	14	AAR34363	Human parathyroid

ALIGNMENTS

RESULT 1

AAR22296

ID AAR22296 standard; Peptide; 34 AA.

XX

AC AAR22296;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Lys 11].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;

KW hypertension.

XX

OS Synthetic.
 XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-29;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

AAU73030

ID AAU73030 standard; Peptide; 34 AA.

XX

AC AAU73030;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #12.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Claim 39; Page 26; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-29;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

AAU73053

ID AAU73053 standard; Peptide; 30 AA.

XX

AC AAU73053;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #35.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and

CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.

XX

SQ Sequence 30 AA;

Query Match 88.2%; Score 30; DB 23; Length 30;

Best Local Similarity 100.0%; Pred. No. 1e-24;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

|||||

Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

RESULT 4

AAU73174

ID AAU73174 standard; Peptide; 35 AA.

XX

AC AAU73174;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #156.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;

KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;

KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;

KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 63; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 35 AA;

Query Match 88.2%; Score 30; DB 23; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.1e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

RESULT 5
 AAW08108

ID AAW08108 standard; peptide; 34 AA.
 XX
 AC AAW08108;
 XX
 DT 10-OCT-1997 (first entry)
 XX
 DE Human parathyroid hormone derivative, [Asp10,Lys11]hPTH(1-34).
 XX
 KW Human; parathyroid hormone; PTH; cAMP-producing activity;
 KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
 KW climacteric disturbance.
 XX

OS Synthetic.
 XX
 PN EP748817-A2.
 XX
 PD 18-DEC-1996.
 XX
 PF 13-JUN-1996; 96EP-0109475.
 XX
 PR 15-JUN-1995; 95JP-0148652.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1997-036114/04.
 XX
 PT New parathyroid hormone derivs. - useful in treatment of bone
 PT diseases, hypoparathyroidism and hypertension
 XX
 PS Claim 27; Page 26; 42pp; English.
 XX
 CC The sequences given in AAW08108-32 represent derivatives of human
 CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
 CC derivative peptides. They have potent cAMP-producing activity and
 CC bone formation activity. They may be used in treatment of bone
 CC diseases including osteoporosis, hypoparathyroidism, hypertension
 CC and climacteric disturbance. The peptides are low in toxicity and
 CC are safe.
 XX
 SQ Sequence 34 AA;

Query Match 70.6%; Score 24; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.5e-18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KGKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 11 KGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

AAR22064

ID AAR22064 standard; Protein; 28 AA.

XX

AC AAR22064;

XX

DT 14-JUL-1992 (first entry)

XX

DE Modified hPTH(7-34)NH2.

XX

KW Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
 KW tumours; hypercalcaemia; renal failure; human.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 7

FT /label= OTHER
 FT /note= "OTHER = see comments"
 FT Modified-site 28
 FT /label= NH2
 XX
 PN US5093233-A.
 XX
 PD 03-MAR-1992.
 XX
 PF 25-APR-1990; 90US-0514394.
 XX
 PR 25-APR-1990; 90US-0514394.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Roubini E, Chorev M, Nutt RF;
 XX
 DR WPI; 1992-096233/12.
 XX
 PT New parathyroid hormone analogues - useful for treatment and in
 PT vitro diagnosis of PTH-dependent tumours, immune disorders,
 PT osteoporosis and hyperparathyroidism.
 XX
 PS Claim 1; Column 10; 6pp; English.
 XX
 CC The peptide is modified at Lys13 (of the parent PTH) in the epsilon
 CC amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH
 CC analogue binds with high affinity to the peptide hormone receptor
 CC without activating the 2nd messenger mol. The modification of the
 CC Lys residue stabilises the bioactive conformation of PTH to enhance
 CC the activity. The peptide may be used in in vitro bioassays to
 CC measure naturally occurring PTH and to diagnose the etiology of or
 CC to treat osteoporosis or hypercalcaemia. It may also be used to
 CC treat hyperthyroidism and diseases caused by aberrant prodn. of
 CC hormone-like substances, such as tumours. It may also be used to
 CC treat immune diseases such as inflammation. It is prepd. by solid
 CC phase synthesis.
 CC See also AAR22058-75.
 XX
 SQ Sequence 28 AA;

 Query Match 67.6%; Score 23; DB 13; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 7
 ABJ10776
 ID ABJ10776 standard; Peptide; 28 AA.
 XX
 AC ABJ10776;
 XX
 DT 02-DEC-2002 (first entry)

XX
 DE Human parathyroid hormone analogue #72.
 XX
 KW Human; parathyroid hormone; parathyroid hormone-related protein;
 KW PTH; PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Modified-site 28
 FT /note= "C-terminal amide"
 XX
 PN W09957139-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 03-MAY-1999; 99WO-US09521.
 XX
 PR 05-MAY-1998; 98US-0072956.
 XX
 PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX
 PI Chorev M, Dong ZX, Rosenblatt M;
 XX
 DR WPI; 2000-038790/03.
 XX
 PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease -
 XX
 PS Claim 11; Page 40; 49pp; English.
 XX
 CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The
 CC present sequence is a peptide analogue of the invention.
 XX
 SQ Sequence 28 AA;

 Query Match 67.6%; Score 23; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 8

AAE23734

ID AAE23734 standard; peptide; 28 AA.

XX

AC AAE23734;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (7-34).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

DR N-PSDB; AAD37995.

XX

PT Regulating mammalian skin or hair cell proliferation and
PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -

XX

PS Claim 35; Fig 38; 56pp; English.

XX

CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.

XX

SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||||
Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 9

AAU73044

ID AAU73044 standard; Peptide; 28 AA.

XX

AC AAU73044;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #26.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for

CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 10

AAE23752

ID AAE23752 standard; peptide; 30 AA.

XX

AC AAE23752;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (5-34).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

XX

PT Regulating mammalian skin or hair cell proliferation and

DR WPI; 2000-476147/41.

XX

PT Differentiating between normal parathyroid function and
PT hyperparathyroidism comprises determining and comparing whole
PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT and/or total parathyroid hormone levels -

XX

PS Disclosure; Page 6; 46pp; English.

XX

CC The present sequence represents an antigenic fragment derived from
CC human parathyroid hormone (PTH). It was used to raise antibodies.
CC PTH peptide fragments can function as PTH antagonists. The
CC specification describes a method for differentiating between a
CC person having substantially normal parathyroid function and having
CC hyperparathyroidism. The method comprises determining and comparing
CC at least two of the following parameters: whole parathyroid
CC hormone level, parathyroid hormone inhibitory peptide fragment level
CC and total parathyroid hormone level. The method is used for monitoring
CC (treatments of) parathyroid related bone disease and the effects of
CC therapeutic treatment for hyperparathyroidism.

XX

SQ Sequence 32 AA;

Query Match 67.6%; Score 23; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 12

AAE23735

ID AAE23735 standard; peptide; 32 AA.

XX

AC AAE23735;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (5-36).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX
 PI Holick MF;
 XX
 DR WPI; 2002-452304/48.
 DR N-PSDB; AAD37995.
 XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein -
 XX
 PS Claim 35; Fig 40; 56pp; English.
 XX
 CC The invention relates to a method for regulating proliferation or
 CC enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX
 SQ Sequence 32 AA;

Query Match 67.6%; Score 23; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.8e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||
 Db 8 GKHLNSMERVEWLRKKLQDVHNF 30

RESULT 13

AAP30022

ID AAP30022 standard; peptide; 34 AA.

XX

AC AAP30022;

XX

DT 25-MAR-2003 (updated)

DT 01-SEP-1992 (first entry)

XX

DE Human parathyroid-(1-34) amide.

XX

KW PTH; parathyroid gland; antibodies.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "amidated"

XX
 PN JP58096052-A.
 XX
 PD 07-JUN-1983.
 XX
 PF 30-NOV-1983; 83JP-0193212.
 XX
 PR 31-MAR-1981; 81JP-0048887.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1983-709291/28.
 XX
 PT High activity human parathyroid hormone amide prodn. - by
 PT condensing protected aminoacid(s) and/or peptide(s) useful for
 PT lowering parathyroid gland function
 XX
 PS Claim 1; Page 1; 20pp; Japanese.
 XX
 CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

AAP50377

ID AAP50377 standard; peptide; 34 AA.

XX

AC AAP50377;

XX

DT 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX

DE [Met(O)8,18]hPTH-(1-34).

XX

KW Human parathyroid hormone; calcium regulation.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /label= oxidised methionine
 FT Modified-site 18
 FT /label= oxidised methionine
 XX
 PN JP59204159-A.
 XX
 PD 19-NOV-1984.
 XX
 PF 28-APR-1983; 83JP-0075607.
 XX
 PR 28-APR-1983; 83JP-0075607.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1985-003560/01.
 XX
 PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.
 XX
 PS Claim 1; Page 1; 3pp; Japanese.
 XX
 CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone
 DE obtainable from a human or animal.

XX

KW Osteoporosis therapy.

XX
 OS Homo sapiens/animal.
 XX
 PN EP197514-A.
 XX
 PD 15-OCT-1986.
 XX
 PF 03-APR-1986; 86EP-0104562.
 XX
 PR 04-APR-1985; 85US-0720018.
 PR 05-DEC-1986; 86US-0939308.
 PR 21-MAY-1987; 87US-0052383.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Potts JT, Neer RM, Slovik DM;
 XX
 DR WPI; 1986-273437/42.
 XX
 PT Compsn. and kits for increasing bone mass in osteoporosis -
 PT contg. parathyroid hormone or fragment with hydroxylated
 PT vitamin/D cpd. or calcium salt
 XX
 PS Claim 4; Page 24; 26pp; English.
 XX
 CC The peptide is used in a pharmaceutical compsn. together with a
 CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
 CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
 CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
 CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

AAR07919

ID AAR07919 standard; protein; 34 AA.

XX

AC AAR07919;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN US4968669-A.
 XX
 PD 06-NOV-1990.
 XX
 PF 21-APR-1989; 89US-0341597.
 XX
 PR 21-APR-1989; 89US-0341597.
 PR 09-MAY-1988; 88US-0191512.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Chorev M;
 XX
 DR WPI; 1990-354642/47.
 XX
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 XX
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

AAR22283

ID AAR22283 standard; peptide; 34 AA.
 XX
 AC AAR22283;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 XX
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX
 OS Homo sapiens.
 XX
 PN WO9204039-A.

XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Holick MF;
 XX
 DR WPI; 1992-114063/14.
 XX
 PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

AAR22292

ID AAR22292 standard; Peptide; 34 AA.
 XX
 AC AAR22292;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1992 (first entry)
 XX
 DE Human parathyroid hormone 1-34 [Phe 11].
 XX
 KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
 KW hypertension.
 XX
 OS Synthetic.

XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

AAR22293

ID AAR22293 standard; Peptide; 34 AA.
 XX
 AC AAR22293;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1992 (first entry)
 XX
 DE Human parathyroid hormone 1-34 [Leu 8].
 XX
 KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
 KW hypertension.
 XX
 OS Synthetic.

XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

AAR22294

ID AAR22294 standard; Peptide; 34 AA.

XX

AC AAR22294;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Ser 11].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
 KW hypertension.

XX

OS Synthetic.

XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

AAR41549

ID AAR41549 standard; protein; 34 AA.

XX

AC AAR41549;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ser3]hPTH (1-34)NH2.

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.

XX

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note = "D-form residue"
 FT Modified-site 34
 FT /note = "C terminal is amidated"
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 22

AAR41550

ID AAR41550 standard; protein; 34 AA.

XX

AC AAR41550;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ala3]hPTH (1-34).

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;

KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note = "D-form residue"
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue has a relative biological activity to hPTH(1-34)
 CC of 2.17.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

AAR41570

ID AAR41570 standard; protein; 34 AA.

XX

AC AAR41570;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [Gln25]hPTH (1-34).

XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 27; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

AAR49697

ID AAR49697 standard; Protein; 34 AA.

XX

AC AAR49697;

XX

DT 14-SEP-1994 (first entry)

XX

DE Sequence of variant of human parathyroid hormone [Ala8]hPTH(1-34).

XX

KW Parathyroid hormone; bone-stimulating; non-vasoactive compound;
 KW osteoporosis; therapy.

XX

OS Synthetic.
 XX
 PN CA2098639-A.
 XX
 PD 20-DEC-1993.
 XX
 PF 17-JUN-1993; 93CA-2098639.
 XX
 PR 19-JUN-1992; 92US-0900680.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzato RP, Kronis KA;
 XX
 DR WPI; 1994-074853/10.
 XX
 PT New Met8-substd. variants of parathyroid hormone - stimulate bone
 PT and are non-vasoactive, useful for treating, e.g. osteoporosis
 XX
 PS Claim 13; Fig 2; 31pp; English.
 XX
 CC AAQ58564 is the sequence of wild-type human parathyroid hormone. In
 CC the cpds of the invention, Met 8 is replaced with Cys, Val or Ala.
 CC In addition, Met 18 may be replaced with Leu. Moreover truncated
 CC variants of 34 AAs with Ala or Cys substituted for Met 8 are also
 CC claimed. The variants have reduced vasoactivity relative to Met 8-
 CC contg. hPTH and are useful for the treatment of bone disorders, such
 CC as osteoporosis. Dosage is 1 microgram - 100 milligram (pref. 1-
 CC microgram - 1000 microgram)/kg.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

AAR49698

ID AAR49698 standard; Protein; 34 AA.

XX

AC AAR49698;

XX

DT 14-SEP-1994 (first entry)

XX

DE Sequence of variant of human parathyroid hormone [Cys8]hPTH(1-34).

XX

KW Parathyroid hormone; bone-stimulating; non-vasoactive compound;
 KW osteoporosis; therapy.

XX

OS Synthetic.

XX

PN CA2098639-A.
 XX
 PD 20-DEC-1993.
 XX
 PF 17-JUN-1993; 93CA-2098639.
 XX
 PR 19-JUN-1992; 92US-0900680.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzato RP, Kronis KA;
 XX
 DR WPI; 1994-074853/10.
 XX
 PT New Met8-substd. variants of parathyroid hormone - stimulate bone
 PT and are non-vasoactive, useful for treating, e.g. osteoporosis
 XX
 PS Claim 14; Fig 2; 31pp; English.
 XX
 CC AAQ58564 is the sequence of wild-type human parathyroid hormone. In
 CC the cpds of the invention, Met 8 is replaced with Cys, Val or Ala.
 CC In addition, Met 18 may be replaced with Leu. Moreover truncated
 CC variants of 34 AAs with Ala or Cys substituted for Met 8 are also
 CC claimed. The variants have reduced vasoactivity relative to Met 8-
 CC contg. hPTH and are useful for the treatment of bone disorders, such
 CC as osteoporosis. Dosage is 1 microgram - 100 milligram (pref. 1-
 CC microgram - 1000 microgram)/kg.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

 RESULT 26
 AAR58291
 ID AAR58291 standard; peptide; 34 AA.
 XX
 AC AAR58291;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Modified-site 26
 FT /label= Other
 FT /note= "Formyl-Lys."
 FT Modified-site 27
 FT /label= Other
 FT /note= "Formyl-Lys."
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 289; Page 47; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 27

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

AC AAR58228;

XX

DT 20-SEP-1994 (first entry)

XX

DE [D-Asp30]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 30

FT /note= "D-form residue."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 226; Page 45; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 28

AAR58016

ID AAR58016 standard; peptide; 34 AA.

XX

AC AAR58016;

XX

DT 20-SEP-1994 (first entry)

XX

DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-alpha-isopropyl-Ser"

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 29

AAR58017

ID AAR58017 standard; peptide; 34 AA.
 XX
 AC AAR58017;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 26
 FT /note= "N-epsilon-Isopropyl-Lys"
 FT Modified-site 27
 FT /note= "N-epsilon-Isopropyl-Lys"
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 2; Page 32; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 30

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;
KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;
KW eicosapentaenoic acid; EPA; antitumor.

XX

OS Synthetic.

XX
 PN WO9412530-A1.
 XX
 PD 09-JUN-1994.
 XX
 PF 29-NOV-1993; 93WO-HU00065.
 XX
 PR 30-NOV-1992; 92US-0984293.
 XX
 PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
 PA (SYNT-) SYNTHETIC PEPTIDES INC.
 XX
 PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;
 PI Szederkenyi F, Vadasz Z;
 XX
 DR WPI; 1994-200194/24.
 XX
 PT New fatty acyl-peptide conjugates for inhibiting cell
 PT proliferation - more active than free peptide, partic. for
 PT treating tumours, virus-infected cells, psoriasis, etc.
 XX
 PS Disclosure; Fig. 1; 45pp; English.
 XX
 CC The peptides given in AAR55718-48 can each be conjugated through an
 CC amide linkage with a polyunsaturated fatty acid moiety, such as
 CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve
 CC antiproliferative activity. The parathormone N-terminal fragment
 CC inhibits osteoblast proliferation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 31

AAR74521

ID AAR74521 standard; Peptide; 34 AA.

XX

AC AAR74521;

XX

DT 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX

DE Human parathyroid hormone (1-34).

XX

KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;

KW osteoporosis; hypercalcaemia; hyperparathroidism;

KW metabolic bone disease; human; veterinary medicine;

KW iontophoretic transdermal transport; recombinant E.coli.

XX

OS Homo sapiens.
 XX
 PN WO9511988-A1.
 XX
 PD 04-MAY-1995.
 XX
 PF 25-OCT-1994; 94WO-US12205.
 XX
 PR 25-OCT-1993; 93US-0142551.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Oldenburg KR, Selick HE;
 XX
 DR WPI; 1995-178880/23.
 XX
 PT New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 XX
 PS Disclosure; Page 1; 109pp; English.
 XX
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (RPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 32
 AAW99449
 ID AAW99449 standard; peptide; 34 AA.
 XX
 AC AAW99449;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Human parathyroid hormone aal-34.
 XX

KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
 KW spontaneous abortion; uterine contraction; human.
 XX
 OS Homo sapiens.
 XX
 PN US5880093-A.
 XX
 PD 09-MAR-1999.
 XX
 PF 05-APR-1995; 95US-0411726.
 XX
 PR 28-SEP-1992; 92IT-MI02331.
 XX
 PA (BAGN/) BAGNOLI F.
 XX
 PI Bagnoli F;
 XX
 DR WPI; 1996-162392/17.
 XX
 PT Use of composition containing parathormone or fragments - for
 PT preventing premature birth or spontaneous abortion or for treating
 PT unwanted uterine contractions
 XX
 PS Disclosure; Column 7-8; 11pp; English.
 XX
 CC Peptides AAW99448-W99452 represent all or part of the parathyroid
 CC hormone (PTH; parathormone) sequence or related peptide. The peptides
 CC are used for preventing premature birth, spontaneous abortion or unwanted
 CC uterine contractions in a pregnant human patient.
 CC (Note: this patent is the first Major Country Equivalent to Italian
 CC Patent IT1255388).
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

AAW15812

ID AAW15812 standard; peptide; 34 AA.

XX

AC AAW15812;

XX

DT 25-MAR-2003 (updated)

DT 05-JUN-1997 (first entry)

XX

DE [Trp(10)]-hPTH(1-34)-OH.

XX

KW human parathyroid hormone; human parathyroid hormone related peptide;

KW hPTH; hPTHrP; antagonist; hyperparathyroidism; hypercalcaemia;

KW tumour; dermatological disorders; hair growth promoter.

XX
 OS Synthetic.
 XX
 PN WO9603437-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 27-JUL-1995; 95WO-EP02993.
 XX
 PR 28-JUL-1994; 94GB-0015255.
 PR 28-JUL-1994; 94GB-0015254.
 XX
 PA (SANO) SANDOZ LTD.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Cardinaux F, Feyen JHM, Gamse R, Gombert FO;
 XX
 DR WPI; 1996-117003/12.
 XX
 PT New parathyroid hormone or parathyroid hormone related peptide cpds.
 PT - useful for preventing or treating conditions associated with
 PT increased plasma calcium, tumour growth and dermatological disorders
 XX
 PS Example 9; Page 9; 32pp; English.
 XX
 CC New parathyroid hormone (PTH) or parathyroid hormone related peptide
 CC (PTHrP) compounds are claimed in which (i) at least one of the amino
 CC acid residues naturally occurring in positions 2 and 10 is replaced
 CC by tryptophan or another amino acid residue bearing an aromatic or
 CC heteroaromatic group on its side chain, and (ii) optionally at least
 CC one of the amino acid residues naturally occurring in positions 3 and 6
 CC is further replaced by tryptophan or another amino acid residue bearing
 CC an aromatic or heteroaromatic group on its side chain. The peptides are
 CC PTH or PTHrP antagonists useful for preventing or treating conditions
 CC associated with increased plasma calcium caused by excessive release of
 CC PTH or PTHrP (e.g. hyperparathyroidism, or hypercalcemia associated with
 CC malignancy); for preventing or treating tumour growth stimulated by
 CC PTHrP; for treating dermatological disorders; and for promoting hair
 CC growth. They may be used in combination with a further active agent,
 CC e.g. a bone resorption inhibitor or cytostatic agent.
 CC The present sequence is a specific example of the new peptides.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34
 AAR99978

ID AAR99978 standard; peptide; 34 AA.
 XX
 AC AAR99978;
 XX
 DT 30-APR-1997 (first entry)
 XX
 DE Human parathyroid hormone peptide fragment (1-34).
 XX
 KW cyclic parathyroid hormone fragment; calcium-regulating activity;
 KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
 KW improved half life; calcium retention; bone.
 XX
 OS Synthetic.
 XX
 PN DE19508672-A1.
 XX
 PD 12-SEP-1996.
 XX
 PF 10-MAR-1995; 95DE-1008672.
 XX
 PR 10-MAR-1995; 95DE-1008672.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
 XX
 DR WPI; 1996-413519/42.
 XX
 PT Cyclic parathyroid hormone fragments with lactam bridge - have good
 PT in vivo half life and are useful for treating osteoporosis and
 PT preventing epidermal cell proliferation
 XX
 PS Disclosure; Page 9; 14pp; German.
 XX
 CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
 CC sequence of h, b, p, r or cPTH(1-34), opt. extended by up to 4 amino
 CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
 CC the N-terminus, and are cyclised between positions 13 and 17. One of
 CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
 CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
 CC treating osteoporosis and inhibit proliferation of epidermal cells (for
 CC treating psoriasis). The CPTH have an improved half life in vivo than
 CC known PTH fragments, increased mitogenicity and DNA-synthesising
 CC capacity, reduced catabolic, calcium-mobilising activity and increased
 CC activity for calcium retention and incorporation into bone. The
 CC present sequence is that of human PTH peptide fragment (1-34).
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

AAR98951

ID AAR98951 standard; peptide; 34 AA.

XX

AC AAR98951;

XX

DT 15-JAN-1997 (first entry)

XX

DE Target peptide (PTH(1-34)) used in fusion protein construct.

XX

KW Fusion protein construct; isolation; purification;
KW growth hormone releasing factor; glucagon-like peptide 1;
KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX

OS Synthetic.

XX

PN WO9617942-A1.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15800.

XX

PR 07-DEC-1994; 94US-0350530.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;

PI Partridge BE, Stout JS, Wagner FW;

XX

DR WPI; 1996-287186/29.

XX

PT Isolation and purificn of peptide(s) from fusion protein constructs

PT - which include a carbonic anhydrase and a variable fused

PT polypeptide

XX

PS Claim 18; Page 48; 67pp; English.

XX

CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a
CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-34 of PTH.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;

KW fusion protein; transpeptidation.

XX

OS Not specified.

XX

PN WO9617941-A2.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15799.

XX

PR 07-DEC-1994; 94US-0350528.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;

PI Wagner FW;

XX

DR WPI; 1996-287185/29.

XX

PT Production of C-terminal alpha-carboxamidated peptide(s) - by

PT cleavage and transpeptidation of recombinant multicopy peptide(s) or

PT fusion constructs

XX

PS Claim 12; Page 70; 93pp; English.

XX

CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be

CC produced as C-terminal amidated peptides utilising novel recombinant

CC protein constructs (see also AAR98967-72) in which single or multiple

CC copies of the peptide are linked by intraconnecting peptides that

CC permit the construct to be selectively reacted to produce product

CC peptides having a C-terminal alpha-carboxamide. Expression cassettes

CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.

CC of the recombinant proteins in transformed E. coli host cells.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

||||||||||||||||||||

RESULT 37

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX

AC AAR88835;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH₂.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10

FT /note= "forms peptide bond with Lys at posn. 26"

FT Modified-site 14

FT /note= "forms peptide bond with Asp at posn. 30"

FT Modified-site 26

FT /note= "forms peptide bond with Asn at posn. 10"

FT Modified-site 30

FT /note= "forms peptide bond with His at posn. 14"

FT Modified-site 34

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 3; Fig 8; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density

CC without undesirable effects. They are useful for the treatment of

CC osteoporosis and other bone related disorders and disorders

CC involving bone cell calcium regulation.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 38

AAW24273

ID AAW24273 standard; protein; 34 AA.

XX

AC AAW24273;

XX

DT 17-OCT-1997 (first entry)

XX

DE Wild type parathyroid hormone.

XX

KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;

KW electrotransportability; alpha-helix; beta-sheet.

XX

OS Homo sapiens.

XX

PN W09639423-A2.

XX

PD 12-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09647.

XX

PR 06-JUN-1995; 95US-0468275.

XX

PA (ALZA) ALZA CORP.

XX

PI Holladay LA, Oldenburg KR;

XX

DR WPI; 1997-043058/04.

XX

PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid

PT hormone and hirulog - which exhibit better or enhanced

PT electro-transportability through a body surface

XX

PS Claim 7; Fig 1A; 55pp; English.

XX

CC The sequences given in AAW24273-76 represent wildtype and analogues of

CC parathyroid hormone (PTH). The analogues exhibit better/enhanced

CC electrotransportability through a body surface, and are characterised

CC by substituting one or more amino acid residues of the parent

CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet

CC segments of the parent polypeptide. An electrotransport device can

CC deliver the polypeptide analogue through a body surface by electro-

CC transport by including providing a therapeutically effective amount

CC of the polypeptide analogue in a donor reservoir of the electrotransport

CC device. The electrotransport flux of a polypeptide is increased by
CC reducing the potential of the polypeptide for forming alpha-helix or
CC beta-sheet segment.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 39

AAW08120

ID AAW08120 standard; peptide; 34 AA.

XX

AC AAW08120;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human PTH derivative, [Aad10]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;
KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW climacteric disturbance.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10

FT /label= Aad

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone
PT diseases, hypoparathyroidism and hypertension

XX

PS Example 1; Page 29; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human
CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and

CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and
CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 40

AAW08109

ID AAW08109 standard; peptide; 34 AA.

XX

AC AAW08109;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human parathyroid hormone derivative, [Glu10]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;

KW bone formation; osteoporosis; hypoparathyroidism; hypertension;

KW climacteric disturbance.

XX

OS Synthetic.

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone

PT diseases, hypoparathyroidism and hypertension

XX

PS Claim 28; Page 26; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human

CC parathyroid hormone (PTH). These peptides are human PTH (1-34)

CC derivative peptides. They have potent cAMP-producing activity and

CC bone formation activity. They may be used in treatment of bone

CC diseases including osteoporosis, hypoparathyroidism, hypertension

CC and climacteric disturbance. The peptides are low in toxicity and

CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34

||||||||||||||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:34:21

Job time : 34.5171 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 11.5452 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	24	70.6	34	3	US-09-044-536A-8
2	23	67.6	33	1	US-08-256-363-1
3	23	67.6	34	1	US-07-765-373-1
4	23	67.6	34	1	US-08-033-099-1
5	23	67.6	34	1	US-08-262-495C-1
6	23	67.6	34	1	US-07-915-247A-1
7	23	67.6	34	1	US-08-443-863-1
8	23	67.6	34	1	US-08-448-070-1
9	23	67.6	34	1	US-08-488-105-7
10	23	67.6	34	1	US-08-468-275-6
11	23	67.6	34	1	US-08-256-363-2

12	23	67.6	34	1	US-08-449-500-1	Sequence 1, Appli
13	23	67.6	34	1	US-08-449-317A-1	Sequence 1, Appli
14	23	67.6	34	2	US-08-142-551B-2	Sequence 2, Appli
15	23	67.6	34	2	US-08-477-022-1	Sequence 1, Appli
16	23	67.6	34	2	US-08-449-447-1	Sequence 1, Appli
17	23	67.6	34	2	US-08-835-231-13	Sequence 13, Appl
18	23	67.6	34	2	US-08-184-328-1	Sequence 1, Appli
19	23	67.6	34	2	US-08-411-726-2	Sequence 2, Appli
20	23	67.6	34	2	US-08-691-647C-5	Sequence 5, Appli
21	23	67.6	34	2	US-08-521-097-1	Sequence 1, Appli
22	23	67.6	34	3	US-09-044-536A-1	Sequence 1, Appli
23	23	67.6	34	3	US-09-044-536A-9	Sequence 9, Appli
24	23	67.6	34	3	US-09-044-536A-10	Sequence 10, Appl
25	23	67.6	34	3	US-09-044-536A-11	Sequence 11, Appl
26	23	67.6	34	3	US-09-044-536A-12	Sequence 12, Appl
27	23	67.6	34	3	US-09-044-536A-13	Sequence 13, Appl
28	23	67.6	34	3	US-09-044-536A-14	Sequence 14, Appl
29	23	67.6	34	3	US-09-044-536A-15	Sequence 15, Appl
30	23	67.6	34	3	US-08-904-760B-22	Sequence 22, Appl
31	23	67.6	34	3	US-09-108-661-13	Sequence 13, Appl
32	23	67.6	34	4	US-09-007-466-6	Sequence 6, Appli
33	23	67.6	34	4	US-09-406-813-1	Sequence 1, Appli
34	23	67.6	34	4	US-08-952-980B-6	Sequence 6, Appli
35	23	67.6	34	4	US-09-228-990-1	Sequence 1, Appli
36	23	67.6	34	4	US-09-447-800-1	Sequence 1, Appli
37	23	67.6	34	4	US-09-447-800-2	Sequence 2, Appli
38	23	67.6	34	4	US-09-447-800-5	Sequence 5, Appli
39	23	67.6	34	4	US-09-447-800-8	Sequence 8, Appli
40	23	67.6	34	4	US-09-536-785A-22	Sequence 22, Appl
41	23	67.6	34	4	US-09-442-989-26	Sequence 26, Appl
42	23	67.6	34	5	PCT-US95-15800-22	Sequence 22, Appl
43	23	67.6	35	1	US-08-256-363-3	Sequence 3, Appli
44	23	67.6	36	1	US-08-112-024-2	Sequence 2, Appli
45	23	67.6	36	1	US-08-256-363-4	Sequence 4, Appli
46	23	67.6	37	1	US-08-440-117-1	Sequence 1, Appli
47	23	67.6	37	3	US-09-068-738A-16	Sequence 16, Appl
48	23	67.6	38	1	US-08-112-024-1	Sequence 1, Appli
49	23	67.6	38	1	US-08-232-849-1	Sequence 1, Appli
50	23	67.6	38	2	US-08-625-586-1	Sequence 1, Appli
51	23	67.6	38	3	US-09-128-401-1	Sequence 1, Appli
52	23	67.6	38	5	PCT-US95-15800-29	Sequence 29, Appl
53	22	64.7	33	4	US-09-447-800-3	Sequence 3, Appli
54	22	64.7	33	4	US-09-447-800-6	Sequence 6, Appli
55	22	64.7	33	4	US-09-447-800-9	Sequence 9, Appli
56	22	64.7	34	3	US-08-903-497A-1	Sequence 1, Appli
57	22	64.7	34	4	US-09-635-076-1	Sequence 1, Appli
58	21	61.8	34	3	US-09-044-536A-26	Sequence 26, Appl
59	21	61.8	34	4	US-09-449-632-24	Sequence 24, Appl
60	20	58.8	31	1	US-08-262-495C-3	Sequence 3, Appli
61	20	58.8	31	2	US-08-691-647C-1	Sequence 1, Appli
62	20	58.8	31	2	US-08-691-647C-6	Sequence 6, Appli
63	20	58.8	31	3	US-08-904-760B-1	Sequence 1, Appli
64	20	58.8	31	3	US-08-904-760B-6	Sequence 6, Appli
65	20	58.8	31	3	US-08-904-760B-14	Sequence 14, Appl
66	20	58.8	31	3	US-08-904-760B-32	Sequence 32, Appl
67	20	58.8	31	4	US-09-406-813-2	Sequence 2, Appli
68	20	58.8	31	4	US-09-536-785A-1	Sequence 1, Appli

69	20	58.8	31	4	US-09-536-785A-6	Sequence 6, Appli
70	20	58.8	31	4	US-09-536-785A-14	Sequence 14, Appl
71	20	58.8	31	4	US-09-536-785A-32	Sequence 32, Appl
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73	19	55.9	30	1	US-08-262-495C-5	Sequence 5, Appli
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75	19	55.9	34	4	US-09-635-076-3	Sequence 3, Appli
76	18	52.9	34	1	US-07-915-247A-2	Sequence 2, Appli
77	18	52.9	34	1	US-08-443-863-2	Sequence 2, Appli
78	18	52.9	34	1	US-08-448-070-2	Sequence 2, Appli
79	18	52.9	34	1	US-08-488-105-2	Sequence 2, Appli
80	18	52.9	34	1	US-08-488-105-8	Sequence 8, Appli
81	18	52.9	34	1	US-08-449-500-2	Sequence 2, Appli
82	18	52.9	34	1	US-08-449-317A-2	Sequence 2, Appli
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86	18	52.9	34	2	US-08-521-097-2	Sequence 2, Appli
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94	17	50.0	34	1	US-08-488-105-14	Sequence 14, Appl
95	17	50.0	34	3	US-09-044-536A-16	Sequence 16, Appl
96	17	50.0	34	3	US-09-044-536A-17	Sequence 17, Appl
97	16	47.1	34	1	US-07-915-247A-3	Sequence 3, Appli
98	16	47.1	34	1	US-08-443-863-3	Sequence 3, Appli
99	16	47.1	34	1	US-08-448-070-3	Sequence 3, Appli
100	16	47.1	34	1	US-08-449-500-3	Sequence 3, Appli
101	16	47.1	34	1	US-08-449-317A-3	Sequence 3, Appli
102	16	47.1	34	2	US-08-477-022-3	Sequence 3, Appli
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104	16	47.1	34	2	US-08-184-328-3	Sequence 3, Appli
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106	15	44.1	28	4	US-09-406-813-3	Sequence 3, Appli
107	15	44.1	29	4	US-09-406-813-4	Sequence 4, Appli
108	15	44.1	30	1	US-08-262-495C-6	Sequence 6, Appli
109	15	44.1	30	3	US-08-904-760B-7	Sequence 7, Appli
110	15	44.1	30	4	US-09-536-785A-7	Sequence 7, Appli
111	15	44.1	31	1	US-08-262-495C-4	Sequence 4, Appli
112	15	44.1	31	2	US-08-691-647C-2	Sequence 2, Appli
113	15	44.1	31	2	US-08-691-647C-3	Sequence 3, Appli
114	15	44.1	31	2	US-08-691-647C-4	Sequence 4, Appli
115	15	44.1	31	3	US-08-904-760B-2	Sequence 2, Appli
116	15	44.1	31	3	US-08-904-760B-3	Sequence 3, Appli
117	15	44.1	31	3	US-08-904-760B-4	Sequence 4, Appli
118	15	44.1	31	3	US-08-904-760B-5	Sequence 5, Appli
119	15	44.1	31	3	US-08-904-760B-8	Sequence 8, Appli
120	15	44.1	31	3	US-08-904-760B-11	Sequence 11, Appl
121	15	44.1	31	3	US-08-904-760B-12	Sequence 12, Appl
122	15	44.1	31	3	US-08-904-760B-15	Sequence 15, Appl
123	15	44.1	31	3	US-08-904-760B-16	Sequence 16, Appl
124	15	44.1	31	3	US-08-904-760B-17	Sequence 17, Appl
125	15	44.1	31	4	US-09-536-785A-2	Sequence 2, Appli

126	15	44.1	31	4	US-09-536-785A-3	Sequence 3, Appli
127	15	44.1	31	4	US-09-536-785A-4	Sequence 4, Appli
128	15	44.1	31	4	US-09-536-785A-5	Sequence 5, Appli
129	15	44.1	31	4	US-09-536-785A-8	Sequence 8, Appli
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131	15	44.1	31	4	US-09-536-785A-12	Sequence 12, Appl
132	15	44.1	31	4	US-09-536-785A-15	Sequence 15, Appl
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135	15	44.1	34	1	US-08-262-495C-2	Sequence 2, Appli
136	15	44.1	34	1	US-08-488-105-4	Sequence 4, Appli
137	15	44.1	34	1	US-08-488-105-6	Sequence 6, Appli
138	15	44.1	34	1	US-08-488-105-10	Sequence 10, Appl
139	15	44.1	34	1	US-08-488-105-11	Sequence 11, Appl
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141	15	44.1	34	1	US-08-488-105-18	Sequence 18, Appl
142	15	44.1	34	1	US-08-449-500-79	Sequence 79, Appl
143	15	44.1	34	1	US-08-449-317A-79	Sequence 79, Appl
144	15	44.1	34	2	US-08-142-551B-3	Sequence 3, Appli
145	15	44.1	34	2	US-08-477-022-79	Sequence 79, Appl
146	15	44.1	34	2	US-08-449-447-79	Sequence 79, Appl
147	15	44.1	34	2	US-08-184-328-79	Sequence 79, Appl
148	15	44.1	34	2	US-08-521-097-79	Sequence 79, Appl
149	15	44.1	34	3	US-09-044-536A-27	Sequence 27, Appl
150	15	44.1	34	3	US-08-904-760B-9	Sequence 9, Appli
151	15	44.1	34	3	US-08-904-760B-10	Sequence 10, Appl
152	15	44.1	34	3	US-08-903-497A-4	Sequence 4, Appli
153	15	44.1	34	4	US-09-635-076-4	Sequence 4, Appli
154	15	44.1	34	4	US-09-536-785A-9	Sequence 9, Appli
155	15	44.1	34	4	US-09-536-785A-10	Sequence 10, Appl
156	15	44.1	35	2	US-08-142-551B-4	Sequence 4, Appli
157	15	44.1	35	2	US-08-142-551B-5	Sequence 5, Appli
158	15	44.1	35	2	US-08-142-551B-7	Sequence 7, Appli
159	15	44.1	35	2	US-08-142-551B-11	Sequence 11, Appl
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167	15	44.1	35	2	US-08-142-551B-19	Sequence 19, Appl
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171	15	44.1	35	2	US-08-142-551B-23	Sequence 23, Appl
172	15	44.1	35	2	US-08-142-551B-24	Sequence 24, Appl
173	15	44.1	35	2	US-08-142-551B-25	Sequence 25, Appl
174	15	44.1	35	2	US-08-142-551B-26	Sequence 26, Appl
175	15	44.1	35	2	US-08-142-551B-27	Sequence 27, Appl
176	15	44.1	35	2	US-08-142-551B-28	Sequence 28, Appl
177	15	44.1	35	2	US-08-142-551B-29	Sequence 29, Appl
178	15	44.1	35	2	US-08-142-551B-30	Sequence 30, Appl
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193	15	44.1	35	2	US-08-142-551B-45	Sequence 45, Appl
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203	15	44.1	35	2	US-08-142-551B-55	Sequence 55, Appl
204	15	44.1	35	2	US-08-142-551B-56	Sequence 56, Appl
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215	15	44.1	35	2	US-08-142-551B-67	Sequence 67, Appl
216	15	44.1	35	2	US-08-142-551B-68	Sequence 68, Appl
217	15	44.1	35	2	US-08-142-551B-70	Sequence 70, Appl
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222	14	41.2	31	3	US-08-904-760B-21	Sequence 21, Appl
223	14	41.2	31	4	US-09-536-785A-21	Sequence 21, Appl
224	14	41.2	34	3	US-09-044-536A-29	Sequence 29, Appl
225	14	41.2	35	2	US-08-142-551B-69	Sequence 69, Appl
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229	14	41.2	35	2	US-08-142-551B-117	Sequence 117, App
230	14	41.2	35	2	US-08-142-551B-118	Sequence 118, App
231	13	38.2	34	1	US-07-773-098-5	Sequence 5, Appli
232	13	38.2	34	1	US-07-773-098-6	Sequence 6, Appli
233	13	38.2	34	3	US-09-044-536A-28	Sequence 28, Appl
234	13	38.2	35	2	US-08-142-551B-72	Sequence 72, Appl
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236	13	38.2	35	2	US-08-142-551B-75	Sequence 75, Appl
237	13	38.2	35	2	US-08-142-551B-111	Sequence 111, App
238	13	38.2	35	2	US-08-142-551B-112	Sequence 112, App
239	13	38.2	35	2	US-08-142-551B-113	Sequence 113, App

240	13	38.2	35	2	US-08-142-551B-114	Sequence 114, App
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242	12	35.3	34	1	US-08-488-105-9	Sequence 9, Appli
243	12	35.3	34	1	US-08-488-105-15	Sequence 15, Appl
244	12	35.3	34	3	US-08-903-497A-5	Sequence 5, Appli
245	12	35.3	34	4	US-09-635-076-5	Sequence 5, Appli
246	12	35.3	35	2	US-08-142-551B-76	Sequence 76, Appl
247	12	35.3	35	2	US-08-142-551B-77	Sequence 77, Appl
248	12	35.3	35	2	US-08-142-551B-78	Sequence 78, Appl
249	12	35.3	35	2	US-08-142-551B-107	Sequence 107, App
250	12	35.3	35	2	US-08-142-551B-108	Sequence 108, App
251	12	35.3	35	2	US-08-142-551B-109	Sequence 109, App
252	12	35.3	35	2	US-08-142-551B-110	Sequence 110, App
253	11	32.4	34	1	US-08-488-105-5	Sequence 5, Appli
254	11	32.4	34	1	US-08-488-105-12	Sequence 12, Appl
255	11	32.4	34	1	US-08-488-105-17	Sequence 17, Appl
256	11	32.4	34	1	US-08-449-500-61	Sequence 61, Appl
257	11	32.4	34	1	US-08-449-317A-61	Sequence 61, Appl
258	11	32.4	34	2	US-08-477-022-61	Sequence 61, Appl
259	11	32.4	34	2	US-08-449-447-61	Sequence 61, Appl
260	11	32.4	34	2	US-08-184-328-61	Sequence 61, Appl
261	11	32.4	34	2	US-08-521-097-61	Sequence 61, Appl
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263	11	32.4	35	2	US-08-142-551B-79	Sequence 79, Appl
264	11	32.4	35	2	US-08-142-551B-81	Sequence 81, Appl
265	11	32.4	35	2	US-08-142-551B-104	Sequence 104, App
266	11	32.4	35	2	US-08-142-551B-105	Sequence 105, App
267	11	32.4	35	2	US-08-142-551B-106	Sequence 106, App
268	11	32.4	35	2	US-08-142-551B-121	Sequence 121, App
269	11	32.4	35	2	US-08-142-551B-122	Sequence 122, App
270	11	32.4	35	2	US-08-142-551B-123	Sequence 123, App
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272	10	29.4	28	4	US-09-448-867-6	Sequence 6, Appli
273	10	29.4	30	3	US-08-904-760B-33	Sequence 33, Appl
274	10	29.4	30	3	US-08-904-760B-34	Sequence 34, Appl
275	10	29.4	30	3	US-08-904-760B-35	Sequence 35, Appl
276	10	29.4	30	4	US-09-536-785A-33	Sequence 33, Appl
277	10	29.4	30	4	US-09-536-785A-34	Sequence 34, Appl
278	10	29.4	30	4	US-09-536-785A-35	Sequence 35, Appl
279	10	29.4	31	3	US-08-904-760B-18	Sequence 18, Appl
280	10	29.4	31	3	US-08-904-760B-19	Sequence 19, Appl
281	10	29.4	31	3	US-08-904-760B-20	Sequence 20, Appl
282	10	29.4	31	4	US-09-406-813-5	Sequence 5, Appli
283	10	29.4	31	4	US-09-536-785A-18	Sequence 18, Appl
284	10	29.4	31	4	US-09-536-785A-19	Sequence 19, Appl
285	10	29.4	31	4	US-09-536-785A-20	Sequence 20, Appl
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287	10	29.4	34	3	US-09-044-536A-21	Sequence 21, Appl
288	10	29.4	34	3	US-09-044-536A-22	Sequence 22, Appl
289	10	29.4	34	3	US-09-044-536A-24	Sequence 24, Appl
290	10	29.4	34	3	US-08-903-497A-6	Sequence 6, Appli
291	10	29.4	34	3	US-08-903-497A-7	Sequence 7, Appli
292	10	29.4	34	4	US-08-952-980B-9	Sequence 9, Appli
293	10	29.4	34	4	US-09-635-076-6	Sequence 6, Appli
294	10	29.4	34	4	US-09-635-076-7	Sequence 7, Appli
295	10	29.4	35	2	US-08-142-551B-82	Sequence 82, Appl
296	10	29.4	35	2	US-08-142-551B-83	Sequence 83, Appl

297	10	29.4	35	2	US-08-142-551B-84	Sequence 84, Appl
298	10	29.4	35	2	US-08-142-551B-101	Sequence 101, App
299	10	29.4	35	2	US-08-142-551B-102	Sequence 102, App
300	10	29.4	35	2	US-08-142-551B-103	Sequence 103, App
301	10	29.4	35	2	US-08-142-551B-120	Sequence 120, App
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303	9	26.5	28	4	US-09-448-867-2	Sequence 2, Appli
304	9	26.5	28	4	US-09-448-867-4	Sequence 4, Appli
305	9	26.5	34	3	US-09-044-536A-2	Sequence 2, Appli
306	9	26.5	34	3	US-09-044-536A-23	Sequence 23, Appl
307	9	26.5	35	2	US-08-142-551B-85	Sequence 85, Appl
308	9	26.5	35	2	US-08-142-551B-86	Sequence 86, Appl
309	9	26.5	35	2	US-08-142-551B-87	Sequence 87, Appl
310	9	26.5	35	2	US-08-142-551B-98	Sequence 98, Appl
311	9	26.5	35	2	US-08-142-551B-99	Sequence 99, Appl
312	9	26.5	35	2	US-08-142-551B-100	Sequence 100, App
313	9	26.5	35	3	US-09-044-536A-30	Sequence 30, Appl
314	9	26.5	36	3	US-09-044-536A-31	Sequence 31, Appl
315	9	26.5	37	3	US-09-044-536A-32	Sequence 32, Appl
316	9	26.5	38	3	US-09-044-536A-33	Sequence 33, Appl
317	9	26.5	39	3	US-09-044-536A-34	Sequence 34, Appl
318	9	26.5	40	3	US-09-044-536A-35	Sequence 35, Appl
319	8	23.5	31	3	US-08-904-760B-13	Sequence 13, Appl
320	8	23.5	31	4	US-09-228-990-50	Sequence 50, Appl
321	8	23.5	31	4	US-09-228-990-51	Sequence 51, Appl
322	8	23.5	31	4	US-09-228-990-66	Sequence 66, Appl
323	8	23.5	31	4	US-09-228-990-67	Sequence 67, Appl
324	8	23.5	31	4	US-09-228-990-76	Sequence 76, Appl
325	8	23.5	31	4	US-09-536-785A-13	Sequence 13, Appl
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329	8	23.5	34	1	US-08-526-987-2	Sequence 2, Appli
330	8	23.5	35	2	US-08-142-551B-88	Sequence 88, Appl
331	8	23.5	35	2	US-08-142-551B-89	Sequence 89, Appl
332	8	23.5	35	2	US-08-142-551B-95	Sequence 95, Appl
333	8	23.5	35	2	US-08-142-551B-96	Sequence 96, Appl
334	8	23.5	35	2	US-08-142-551B-97	Sequence 97, Appl
335	7	20.6	28	4	US-09-228-990-65	Sequence 65, Appl
336	7	20.6	28	4	US-09-228-990-78	Sequence 78, Appl
337	7	20.6	28	4	US-09-228-990-79	Sequence 79, Appl
338	7	20.6	28	4	US-09-442-989-22	Sequence 22, Appl
339	7	20.6	28	4	US-09-442-989-24	Sequence 24, Appl
340	7	20.6	28	4	US-09-442-989-25	Sequence 25, Appl
341	7	20.6	29	4	US-09-406-813-8	Sequence 8, Appli
342	7	20.6	31	4	US-09-406-813-9	Sequence 9, Appli
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345	7	20.6	34	1	US-08-033-099-2	Sequence 2, Appli
346	7	20.6	34	1	US-08-468-275-7	Sequence 7, Appli
347	7	20.6	34	1	US-08-468-275-8	Sequence 8, Appli
348	7	20.6	34	1	US-08-449-500-37	Sequence 37, Appl
349	7	20.6	34	1	US-08-449-317A-37	Sequence 37, Appl
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351	7	20.6	34	2	US-08-449-447-37	Sequence 37, Appl
352	7	20.6	34	2	US-08-184-328-37	Sequence 37, Appl
353	7	20.6	34	2	US-08-521-097-37	Sequence 37, Appl

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355	7	20.6	34	4	US-09-007-466-8	Sequence 8, Appli
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362	7	20.6	35	2	US-08-142-551B-91	Sequence 91, Appl
363	7	20.6	35	2	US-08-142-551B-92	Sequence 92, Appl
364	7	20.6	35	2	US-08-142-551B-93	Sequence 93, Appl
365	7	20.6	35	2	US-08-142-551B-124	Sequence 124, App
366	7	20.6	35	4	US-08-952-980B-7	Sequence 7, Appli
367	7	20.6	35	4	US-08-952-980B-8	Sequence 8, Appli
368	6	17.6	28	4	US-09-228-990-54	Sequence 54, Appl
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373	6	17.6	30	4	US-09-228-990-64	Sequence 64, Appl
374	6	17.6	30	4	US-09-536-785A-23	Sequence 23, Appl
375	6	17.6	31	3	US-08-904-760B-23	Sequence 23, Appl
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379	6	17.6	31	4	US-09-228-990-5	Sequence 5, Appli
380	6	17.6	31	4	US-09-228-990-6	Sequence 6, Appli
381	6	17.6	31	4	US-09-228-990-7	Sequence 7, Appli
382	6	17.6	31	4	US-09-228-990-8	Sequence 8, Appli
383	6	17.6	31	4	US-09-228-990-9	Sequence 9, Appli
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387	6	17.6	31	4	US-09-228-990-13	Sequence 13, Appl
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389	6	17.6	31	4	US-09-228-990-15	Sequence 15, Appl
390	6	17.6	31	4	US-09-228-990-16	Sequence 16, Appl
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393	6	17.6	31	4	US-09-228-990-19	Sequence 19, Appl
394	6	17.6	31	4	US-09-228-990-20	Sequence 20, Appl
395	6	17.6	31	4	US-09-228-990-21	Sequence 21, Appl
396	6	17.6	31	4	US-09-228-990-22	Sequence 22, Appl
397	6	17.6	31	4	US-09-228-990-23	Sequence 23, Appl
398	6	17.6	31	4	US-09-228-990-24	Sequence 24, Appl
399	6	17.6	31	4	US-09-228-990-25	Sequence 25, Appl
400	6	17.6	31	4	US-09-228-990-26	Sequence 26, Appl
401	6	17.6	31	4	US-09-228-990-27	Sequence 27, Appl
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430	6	17.6	31	4	US-09-228-990-82	Sequence 82, Appl
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467	5	14.7	29	1	US-08-646-715-33	Sequence 33, Appl

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512	5	14.7	39	1	US-07-778-926-16	Sequence 16, Appl
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517	4	11.8	28	2	US-08-185-949B-76	Sequence 76, Appl
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519	4	11.8	28	2	US-08-818-253-22	Sequence 22, Appl
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523	4	11.8	28	4	US-09-316-919-38	Sequence 38, Appl
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526	4	11.8	29	4	US-09-227-357-480	Sequence 480, App
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530	4	11.8	30	1	US-08-305-799A-4	Sequence 4, Appli
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533	4	11.8	31	1	US-08-340-812-3	Sequence 3, Appli
534	4	11.8	31	1	US-08-248-021A-5	Sequence 5, Appli
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538	4	11.8	31	1	US-08-198-094-44	Sequence 44, Appl
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549	4	11.8	31	3	US-08-107-794A-62	Sequence 62, Appl
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557	4	11.8	31	5	PCT-US95-02087-62	Sequence 62, Appl
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561	4	11.8	32	1	US-08-190-802A-114	Sequence 114, App
562	4	11.8	32	1	US-08-190-802A-183	Sequence 183, App
563	4	11.8	32	1	US-08-190-802A-216	Sequence 216, App
564	4	11.8	32	3	US-08-477-346-110	Sequence 110, App
565	4	11.8	32	3	US-08-477-346-114	Sequence 114, App
566	4	11.8	32	3	US-08-477-346-183	Sequence 183, App
567	4	11.8	32	3	US-08-477-346-216	Sequence 216, App
568	4	11.8	32	4	US-08-473-089-110	Sequence 110, App
569	4	11.8	32	4	US-08-473-089-114	Sequence 114, App
570	4	11.8	32	4	US-08-473-089-183	Sequence 183, App
571	4	11.8	32	4	US-08-473-089-216	Sequence 216, App
572	4	11.8	32	4	US-09-149-476-442	Sequence 442, App
573	4	11.8	32	4	US-08-487-072A-110	Sequence 110, App
574	4	11.8	32	4	US-08-487-072A-114	Sequence 114, App
575	4	11.8	32	4	US-08-487-072A-183	Sequence 183, App
576	4	11.8	32	4	US-08-487-072A-216	Sequence 216, App
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579	4	11.8	33	3	US-09-023-731-16	Sequence 16, Appl
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581	4	11.8	33	4	US-09-122-144-4	Sequence 4, Appli

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586	4	11.8	34	1	US-08-485-607-7	Sequence 7, Appli
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588	4	11.8	34	4	US-09-433-043B-7	Sequence 7, Appli
589	4	11.8	35	4	US-09-227-357-486	Sequence 486, App
590	4	11.8	35	4	US-09-690-454-138	Sequence 138, App
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609	4	11.8	38	2	US-08-378-548-12	Sequence 12, Appl
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654	3	8.8	28	1	US-07-690-300B-79	Sequence 79, Appl
655	3	8.8	28	1	US-07-690-300B-82	Sequence 82, Appl
656	3	8.8	28	1	US-07-690-300B-88	Sequence 88, Appl
657	3	8.8	28	1	US-07-690-300B-91	Sequence 91, Appl
658	3	8.8	28	1	US-07-690-300B-93	Sequence 93, Appl
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662	3	8.8	28	1	US-07-833-468-1	Sequence 1, Appli
663	3	8.8	28	1	US-08-052-681-10	Sequence 10, Appl
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667	3	8.8	28	1	US-08-201-092-2	Sequence 2, Appli
668	3	8.8	28	1	US-08-055-530-29	Sequence 29, Appl
669	3	8.8	28	1	US-08-122-578-1	Sequence 1, Appli
670	3	8.8	28	1	US-08-255-558B-6	Sequence 6, Appli
671	3	8.8	28	1	US-08-117-080-9	Sequence 9, Appli
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675	3	8.8	28	1	US-08-246-572-5	Sequence 5, Appli
676	3	8.8	28	1	US-08-190-802A-84	Sequence 84, Appl
677	3	8.8	28	1	US-08-361-443-1	Sequence 1, Appli
678	3	8.8	28	1	US-08-311-611A-12	Sequence 12, Appl
679	3	8.8	28	1	US-08-311-611A-56	Sequence 56, Appl
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682	3	8.8	28	1	US-08-311-611A-195	Sequence 195, App
683	3	8.8	28	1	US-08-311-611A-196	Sequence 196, App
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686	3	8.8	28	1	US-08-194-591-1	Sequence 1, Appli
687	3	8.8	28	1	US-08-194-591-2	Sequence 2, Appli
688	3	8.8	28	1	US-08-257-446-6	Sequence 6, Appli
689	3	8.8	28	1	US-08-372-783-12	Sequence 12, Appl
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691	3	8.8	28	1	US-08-372-783-193	Sequence 193, App
692	3	8.8	28	1	US-08-372-783-194	Sequence 194, App
693	3	8.8	28	1	US-08-372-783-195	Sequence 195, App
694	3	8.8	28	1	US-08-372-783-196	Sequence 196, App
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699	3	8.8	28	1	US-08-366-591-12	Sequence 12, Appl
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775	3	8.8	28	1	US-08-308-729-72	Sequence 72, Appl
776	3	8.8	28	1	US-08-308-729-73	Sequence 73, Appl
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803	3	8.8	28	1	US-08-615-279-16	Sequence 16, Appl
804	3	8.8	28	1	US-08-615-279-39	Sequence 39, Appl
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807	3	8.8	28	2	US-08-449-447-81	Sequence 81, Appl
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814	3	8.8	28	2	US-08-621-803-143	Sequence 143, App
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820	3	8.8	28	2	US-08-485-445A-196	Sequence 196, App
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837	3	8.8	28	2	US-08-821-619-10	Sequence 10, Appl
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919	3	8.8	28	3	US-09-224-480-196	Sequence 196, App
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943	3	8.8	28	3	US-08-485-264A-136	Sequence 136, App
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949	3	8.8	28	3	US-09-041-886-39	Sequence 39, Appl
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956	3	8.8	28	3	US-09-041-886-56	Sequence 56, Appl
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962	3	8.8	28	3	US-08-894-327-22	Sequence 22, Appl
963	3	8.8	28	3	US-09-082-279B-54	Sequence 54, Appl
964	3	8.8	28	3	US-09-082-279B-62	Sequence 62, Appl
965	3	8.8	28	3	US-09-082-279B-982	Sequence 982, App
966	3	8.8	28	3	US-09-082-279B-1279	Sequence 1279, Ap
967	3	8.8	28	3	US-09-082-279B-1280	Sequence 1280, Ap
968	3	8.8	28	3	US-09-082-279B-1314	Sequence 1314, Ap
969	3	8.8	28	3	US-09-082-279B-1315	Sequence 1315, Ap
970	3	8.8	28	3	US-08-477-346-84	Sequence 84, Appl
971	3	8.8	28	3	US-09-127-926-8	Sequence 8, Appli
972	3	8.8	28	3	US-09-127-926-17	Sequence 17, Appl
973	3	8.8	28	3	US-09-127-926-18	Sequence 18, Appl
974	3	8.8	28	3	US-09-127-926-19	Sequence 19, Appl
975	3	8.8	28	3	US-09-127-926-21	Sequence 21, Appl
976	3	8.8	28	3	US-09-127-926-22	Sequence 22, Appl
977	3	8.8	28	3	US-08-894-997-43	Sequence 43, Appl
978	3	8.8	28	3	US-09-217-352-30	Sequence 30, Appl
979	3	8.8	28	3	US-09-217-352-139	Sequence 139, App
980	3	8.8	28	3	US-09-217-352-140	Sequence 140, App

981	3	8.8	28	3	US-09-217-352-142	Sequence 142, App
982	3	8.8	28	3	US-09-217-352-143	Sequence 143, App
983	3	8.8	28	3	US-09-019-095A-34	Sequence 34, Appl
984	3	8.8	28	4	US-09-406-781-10	Sequence 10, Appl
985	3	8.8	28	4	US-09-406-781-11	Sequence 11, Appl
986	3	8.8	28	4	US-09-260-846-16	Sequence 16, Appl
987	3	8.8	28	4	US-08-474-349A-84	Sequence 84, Appl
988	3	8.8	28	4	US-08-474-349A-136	Sequence 136, App
989	3	8.8	28	4	US-09-099-041A-23	Sequence 23, Appl
990	3	8.8	28	4	US-09-187-789-23	Sequence 23, Appl
991	3	8.8	28	4	US-08-473-089-84	Sequence 84, Appl
992	3	8.8	28	4	US-09-227-357-481	Sequence 481, App
993	3	8.8	28	4	US-09-227-357-531	Sequence 531, App
994	3	8.8	28	4	US-09-315-304B-54	Sequence 54, Appl
995	3	8.8	28	4	US-09-315-304B-62	Sequence 62, Appl
996	3	8.8	28	4	US-09-315-304B-982	Sequence 982, App
997	3	8.8	28	4	US-09-315-304B-1279	Sequence 1279, Ap
998	3	8.8	28	4	US-09-315-304B-1280	Sequence 1280, Ap
999	3	8.8	28	4	US-09-315-304B-1314	Sequence 1314, Ap
1000	3	8.8	28	4	US-09-315-304B-1315	Sequence 1315, Ap

ALIGNMENTS

RESULT 1

US-09-044-536A-8

; Sequence 8, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

```

; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-8

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Query Match          70.6%; Score 24; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 KGKHLNSMERVEWLRKKLQDVHNF 34
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Db      11 KGKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 2

US-08-256-363-1

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; Sequence 1, Application US/08256363
; Patent No. 5783558
; GENERAL INFORMATION:
; APPLICANT: DUVOS, CHRISTIAN
; APPLICANT: MAYER, HUBERT
; APPLICANT: MUELLER-BECKMANN, BERND
; APPLICANT: STREIN, KLAUS
; APPLICANT: WINGENDER, EDGAR
; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR
; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELESTEIN, MURRAY, AND ORAM
; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 2005 5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,363
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 03 040.4
; FILING DATE: 04-FEB-1992

```

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00259
 ; FILING DATE: 04-FEB-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KLESNER, SHARON N.
 ; REGISTRATION NUMBER: 36,335
 ; REFERENCE/DOCKET NUMBER: P1614-4025
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 638-5000
 ; TELEFAX: (202) 638-4810
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-256-363-1

Query Match 67.6%; Score 23; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.3e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
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 Db 10 GKHLNSMERVEWLRKKLQDVHNF 32

RESULT 3

US-07-765-373-1

; Sequence 1, Application US/07765373
 ; Patent No. 5393869
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: KAWASE, Masahiro
 ; APPLICANT: YAMAZAKI, Iwao
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/765,373
 ; FILING DATE: 19910925
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, Gregory D.
 ; REGISTRATION NUMBER: 30901
 ; REFERENCE/DOCKET NUMBER: 41289
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; TELEX: 20091 STRE UR
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 US-07-765-373-1

Query Match 67.6%; Score 23; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 4

US-08-033-099-1

; Sequence 1, Application US/08033099
 ; Patent No. 5434246
 ; GENERAL INFORMATION:
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: TAKETOMI, Shigehisa
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G.CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/033,099
 ; FILING DATE: 19930316
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILLIAMS, Gregory D
 ; REGISTRATION NUMBER: 30901
 ; REFERENCE/DOCKET NUMBER: 42528
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-495C-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

US-07-915-247A-1

; Sequence 1, Application US/07915247A

; Patent No. 5589452

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/915,247A

; FILING DATE: 19920714

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-07-915-247A-1

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Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
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 Db 12 GKHLNSMERVEWLRKKLODVHNF 34

RESULT 7

US-08-443-863-1

; Sequence 1, Application US/08443863

; Patent No. 5693616

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

APPLICANT: Nestor Jr., John J.

APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

10 TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

STREET: 3401 Hillview Ave.

CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

ZIP: 94303

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/443,863

FILING DATE: 14-JUL-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-6593

TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

US-08-443-863-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-08-448-070-1

; Sequence 1, Application US/08448070

; Patent No. 5695955

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/448,070

; FILING DATE: 14-JUL-1992

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-448-070-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

US-08-488-105-7

; Sequence 7, Application US/08488105

; Patent No. 5717062

; GENERAL INFORMATION:

; APPLICANT: Chorev, Michael

; APPLICANT: Rosenblatt, Michael

; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,105

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Tsao, Y. Rocky

; REGISTRATION NUMBER: 34,053

; REFERENCE/DOCKET NUMBER: 00537/112001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; OTHER INFORMATION: The side chains of Lys at
; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an
amide bond,
; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,
CONH2), rather
; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
US-08-488-105-7

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 10

US-08-468-275-6

; Sequence 6, Application US/08468275

; Patent No. 5747453

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94303-0802

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,275

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLER, D. BYRON

; REGISTRATION NUMBER: 30,661

; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 496-8150

; TELEFAX: (415) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-468-275-6

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 11

US-08-256-363-2

; Sequence 2, Application US/08256363
; Patent No. 5783558
; GENERAL INFORMATION:
; APPLICANT: DUVOS, CHRISTIAN
; APPLICANT: MAYER, HUBERT
; APPLICANT: MUELLER-BECKMANN, BERND
; APPLICANT: STREIN, KLAUS
; APPLICANT: WINGENDER, EDGAR
; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR
; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARCELSTEIN, MURRAY, AND ORAM
; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 2005 5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,363
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 03 040.4
; FILING DATE: 04-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00259
; FILING DATE: 04-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KLESNER, SHARON N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: P1614-4025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-363-2

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 10 GKHLNSMERVEWLRKKLQDVHNF 32

RESULT 12

US-08-449-500-1

; Sequence 1, Application US/08449500
; Patent No. 5798225

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,500
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-500-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

US-08-449-317A-1

; Sequence 1, Application US/08449317A
; Patent No. 5807823
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,317A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;

; LOCATION: 1..34
; OTHER INFORMATION: /note= "The sequence of the 34
; OTHER INFORMATION: amino acid truncated human PTH peptide,
; OTHER INFORMATION: designated: Human PTH."
US-08-142-551B-2

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-08-477-022-1

; Sequence 1, Application US/08477022
; Patent No. 5821225
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,022
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

US-08-477-022-1

Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-08-835-231-13

; Sequence 13, Application US/08835231

; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 5861284uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

; APPLICATION NUMBER: JP 024841

; FILING DATE: 19-FEB-1991

; APPLICATION NUMBER: JP 0271438

; FILING DATE: 18-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41614-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-13

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-08-184-328-1

; Sequence 1, Application US/08184328

; Patent No. 5874086

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/184,328

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-184-328-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-08-411-726-2

; Sequence 2, Application US/08411726

; Patent No. 5880093

; GENERAL INFORMATION:

; APPLICANT: BAGNOLI, Franco

; TITLE OF INVENTION: Use of Parathormone, Its Biologically

; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The
Preparation of

; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment
of Pregnanc

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenyon & Kenyon

; STREET: 1 Broadway

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

; SOFTWARE: WordPerfect 6.1 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,726

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/02755

; FILING DATE: 08-OCT-1993

; APPLICATION NUMBER: MI-92A002331

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: PALMESE, Maria Luisa

; REGISTRATION NUMBER: 34,402

; REFERENCE/DOCKET NUMBER: 2111/1300

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-425-7200

; TELEFAX: 212-425-5288

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-2

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

US-08-691-647C-5

; Sequence 5, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue; 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C

; FILING DATE: August 2, 1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-5

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-08-521-097-1

; Sequence 1, Application US/08521097

; Patent No. 5977070

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/521,097

; FILING DATE: 29-AUG-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,328

; FILING DATE: 18-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-521-097-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 22

US-09-044-536A-1

; Sequence 1, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-1

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

US-09-044-536A-9

; Sequence 9, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-9

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

US-09-044-536A-10

; Sequence 10, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-10

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

US-09-044-536A-11

; Sequence 11, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-11

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 26

US-09-044-536A-12

; Sequence 12, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

```

;     TYPE:  amino acid
;     STRANDEDNESS:
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;     NAME/KEY:  partial peptide
;     LOCATION:  1..34
;     FEATURE:
;     NAME/KEY:  Modified-site
;     LOCATION:  11
;     OTHER INFORMATION:  /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12

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Query Match          67.6%;  Score 23;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-16;
Matches   23;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
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Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 27

US-09-044-536A-13

; Sequence 13, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400


```

; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "Xaa=4-carboxyglutamic
; OTHER INFORMATION: acid"
US-09-044-536A-13

```

```

Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        |||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 28

US-09-044-536A-14

```

; Sequence 14, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:

```

; NAME: CONLIN, David G
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 46509-DIV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: partial peptide
 ; LOCATION: 1..34
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 10
 ; OTHER INFORMATION: /product= "Xaa=2-aminosuberic acid"
 US-09-044-536A-14

Query Match 67.6%; Score 23; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 29

US-09-044-536A-15

; Sequence 15, Application US/09044536A
 ; Patent No. 6025467
 ; GENERAL INFORMATION:
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: HABASHITA, Junko
 ; APPLICANT: TAKETOMI, Shigehisa
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/044,536A
 ; FILING DATE: 19-MAR-1998

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "2-aminoadipic acid"
US-09-044-536A-15

```

```

Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 30

US-08-904-760B-22

```

; Sequence 22, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/904,760B
;      FILING DATE:  01-AUG-1997
;      CLASSIFICATION:  514
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/691,647
;      FILING DATE:  02-AUG-1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Crawford, Arthur R.
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  1339-6
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4000
;      TELEFAX:  703-816-4100
;      INFORMATION FOR SEQ ID NO:  22:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-904-760B-22

```

```

Query Match          67.6%;  Score 23;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-16;
Matches   23;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

QY      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 31

US-09-108-661-13

```

; Sequence 13, Application US/09108661
; Patent No. 6287806
; GENERAL INFORMATION:
; APPLICANT:  NISHIMURA, Osamu
; APPLICANT:  KURIYAMA, Masato
; APPLICANT:  KOYAMA, No. 6287806uyuki
; APPLICANT:  FUKUDA, Tsunehiko
; TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES:  37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET:  130 WATER STREET
; CITY:  BOSTON
; STATE:  MA
; COUNTRY:  USA
; ZIP:  02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Diskette
; COMPUTER:  IBM Compatible

```

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/108,661
;   FILING DATE:
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/350,709
;   FILING DATE:  07-DEC-1994
;   APPLICATION NUMBER:  07/838,857
;   FILING DATE:  18-FEB-1992
;   APPLICATION NUMBER:  JP 024841
;   FILING DATE:  19-FEB-1991
;   APPLICATION NUMBER:  JP 0271438
;   FILING DATE:  18-OCT-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  DAVID, RESNICK S
;   REGISTRATION NUMBER:  34,235
;   REFERENCE/DOCKET NUMBER:  41614-FWC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  617-523-3400
;   TELEFAX:  617-523-6440
;   TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  13:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  34 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FRAGMENT TYPE:  N-terminal
;   ORIGINAL SOURCE:
US-09-108-661-13

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Query Match          67.6%;  Score 23;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-16;
Matches  23;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

```

RESULT 32
US-09-007-466-6
; Sequence 6, Application US/09007466
; Patent No. 6313092
; GENERAL INFORMATION:
;   APPLICANT:  HOLLADAY, LESLIE A.
;   APPLICANT:  OLDENBURG, KEVIN R.
;   TITLE OF INVENTION:  METHOD FOR INCREASING THE
;   TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;   NUMBER OF SEQUENCES:  10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  ALZA CORPORATION

```

; STREET: 950 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94303-0802
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/007,466
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/468,275
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MILLER, D. BYRON
 ; REGISTRATION NUMBER: 30,661
 ; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 496-8150
 ; TELEFAX: (415) 496-8048
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-007-466-6

Query Match 67.6%; Score 23; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

US-09-406-813-1

; Sequence 1, Application US/09406813
 ; Patent No. 6316410
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbier, Jean-Rene
 ; APPLICANT: Morley, Paul
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 10688-1B
 ; CURRENT APPLICATION NUMBER: US/09/406,813
 ; CURRENT FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: 08/904,760

; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-406-813-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34

US-08-952-980B-6

; Sequence 6, Application US/08952980B

; Patent No. 6333189

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94303-0802

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/952,980B

; FILING DATE: 20-NOV-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLER, D. BYRON

; REGISTRATION NUMBER: 30,661

; REFERENCE/DOCKET NUMBER: 2349 CIP 1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 496-8150

; TELEFAX: (650) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-952-980B-6

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

US-09-228-990-1

; Sequence 1, Application US/09228990
; Patent No. 6472505

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.
; APPLICANT: Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/228,990
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

US-09-228-990-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

US-09-447-800-1
; Sequence 1, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-09-447-800-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 37

US-09-447-800-2
; Sequence 2, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800

; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-09-447-800-2

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 38

US-09-447-800-5

; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 39

US-09-447-800-8

; Sequence 8, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-09-447-800-8

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 40

US-09-536-785A-22

; Sequence 22, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01

; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-536-785A-22

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:43:31
Job time : 13.5452 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 10.0623 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	5	14.7	34	2	A84241	hypothetical prote	
2	5	14.7	34	2	B97032	transcription regu	
3	5	14.7	35	2	E95098	hypothetical prote	
4	4	11.8	28	2	T09594	gene LFY protein -	
5	4	11.8	29	1	A55527	pyrroloquinoline q	
6	4	11.8	29	2	S01614	dystrophin - rat (
7	4	11.8	29	2	I78537	copper transportin	
8	4	11.8	29	2	S78412	ribosomal protein	
9	4	11.8	30	2	S63531	hypothetical prote	
10	4	11.8	31	2	S44471	glucagon G1 - Nort	
11	4	11.8	31	2	S44472	glucagon G2 - Nort	
12	4	11.8	31	2	D70236	hypothetical prote	
13	4	11.8	32	2	F23454	ovalbumin phosphos	

14	4	11.8	32	2	D31461	T-cell receptor de
15	4	11.8	32	2	G84161	hypothetical prote
16	4	11.8	33	2	E81714	hypothetical prote
17	4	11.8	35	2	D23454	ovalbumin phosphos
18	4	11.8	35	2	G23454	ovalbumin phosphos
19	4	11.8	35	2	D82125	hypothetical prote
20	4	11.8	36	2	S70806	hypothetical prote
21	4	11.8	36	2	F95057	hypothetical prote
22	4	11.8	36	2	A84774	hypothetical prote
23	4	11.8	36	2	S46227	hypothetical prote
24	4	11.8	37	2	S71912	hemoglobin, extrac
25	4	11.8	37	2	T12635	homeotic protein H
26	4	11.8	37	2	A43933	antigen 5 epitope
27	4	11.8	39	1	CKFHCS	sarcotoxin IC - fl
28	4	11.8	39	2	S71913	hemoglobin, extrac
29	4	11.8	39	2	S77164	ycf32 protein - Sy
30	3	8.8	28	2	A42272	brain-type creatin
31	3	8.8	28	2	C32416	phospholipase A2 (
32	3	8.8	28	2	B60071	vasoactive intesti
33	3	8.8	28	2	A60304	vasoactive intesti
34	3	8.8	28	2	S58386	T-cell receptor be
35	3	8.8	28	2	S10052	ribosomal protein
36	3	8.8	28	2	A60752	outer membrane pro
37	3	8.8	28	2	S56121	type I DNA methylt
38	3	8.8	28	2	S70894	hypothetical prote
39	3	8.8	28	2	S22469	hypothetical prote
40	3	8.8	28	2	C60683	malate dehydrogena
41	3	8.8	28	2	S06668	toxin-like protein
42	3	8.8	28	2	S26254	rel protein - chic
43	3	8.8	28	2	I59477	antigen, T-cell re
44	3	8.8	28	2	F46522	T-cell receptor et
45	3	8.8	28	2	H85908	hypothetical prote
46	3	8.8	29	1	GCCB	glucagon - Chinch
47	3	8.8	29	2	S39968	probable hydro-lya
48	3	8.8	29	2	S17147	galanin - chicken
49	3	8.8	29	2	JH0699	omega-conotoxin MV
50	3	8.8	29	2	T44245	ribosomal protein
51	3	8.8	29	2	A05272	gelsolin, cytosoli
52	3	8.8	29	2	B44101	calmodulin, vasoac
53	3	8.8	29	2	S42642	probable rhicadhes
54	3	8.8	29	2	A00774	3-oxoadipate enol-
55	3	8.8	29	2	I84189	cyclic AMP recepto
56	3	8.8	29	2	S65747	CDP-paratose synth
57	3	8.8	29	2	S65748	CDP-paratose synth
58	3	8.8	29	2	B41476	probable antigen 2
59	3	8.8	29	2	T31443	cytochrome bc chai
60	3	8.8	29	2	F85570	hypothetical prote
61	3	8.8	29	2	I49732	NADH2 dehydrogenas
62	3	8.8	30	2	S40309	tyrosine 3-monooxy
63	3	8.8	30	2	C21897	ornithine carbamoy
64	3	8.8	30	2	A05315	pancreatic ribonuc
65	3	8.8	30	2	A61333	trypsin (EC 3.4.21
66	3	8.8	30	2	S21815	H+-exporting ATPas
67	3	8.8	30	2	A44912	cysteine proteinas
68	3	8.8	30	2	B61125	glucagon-like pept
69	3	8.8	30	2	C61125	glucagon-like pept
70	3	8.8	30	2	F32502	T-cell receptor de

71	3	8.8	30	2	PD0013	cAMP response elem
72	3	8.8	30	2	S11617	ribosomal protein
73	3	8.8	30	2	S21195	spectrin beta chai
74	3	8.8	30	2	PC4172	profilin - rat (fr
75	3	8.8	30	2	A34461	heat shock protein
76	3	8.8	30	2	A22977	delta-endotoxin -
77	3	8.8	30	2	S08565	ribulose-bisphosph
78	3	8.8	30	2	S30333	N-carbamoyl-D-amin
79	3	8.8	30	2	PQ0444	hypothetical prote
80	3	8.8	30	2	B95020	hypothetical prote
81	3	8.8	30	2	H95021	hypothetical prote
82	3	8.8	30	2	D72276	hypothetical prote
83	3	8.8	30	2	D70253	conserved hypothet
84	3	8.8	30	2	B70165	hypothetical prote
85	3	8.8	30	2	C81791	hypothetical prote
86	3	8.8	30	2	E82294	hypothetical prote
87	3	8.8	30	2	D82251	hypothetical prote
88	3	8.8	30	2	F82209	hypothetical prote
89	3	8.8	30	2	S72626	small-cell-variant
90	3	8.8	30	2	A35687	probable 39K inorg
91	3	8.8	30	2	A32946	trypsin-like serin
92	3	8.8	30	2	S65519	carcinoembryonic a
93	3	8.8	30	2	S34765	4-hydroxybutyryl-C
94	3	8.8	30	2	D81532	hypothetical prote
95	3	8.8	30	2	A48923	retrovirus-related
96	3	8.8	30	2	B56586	storage hexamer 2
97	3	8.8	30	2	F81360	very hypothetical
98	3	8.8	30	2	S15650	NADH2 dehydrogenas
99	3	8.8	30	2	H97596	hypothetical prote
100	3	8.8	30	4	I52605	hypothetical MLL/E
101	3	8.8	31	2	T44925	hypothetical prote
102	3	8.8	31	2	S39019	glucagon-like pept
103	3	8.8	31	2	A58793	relaxin chain B -
104	3	8.8	31	2	A58586	conotoxin MrVIA -
105	3	8.8	31	2	F30608	Ig kappa chain V-I
106	3	8.8	31	2	D30608	Ig kappa chain V-I
107	3	8.8	31	2	F31461	T-cell receptor de
108	3	8.8	31	2	S03295	Ig alpha chain C r
109	3	8.8	31	2	S03297	Ig alpha chain C r
110	3	8.8	31	2	I52232	tau protein - huma
111	3	8.8	31	2	A36162	neutrophil-activat
112	3	8.8	31	2	S04980	ferritin heavy cha
113	3	8.8	31	2	S32610	antiviral protein
114	3	8.8	31	2	S38881	inner membrane pro
115	3	8.8	31	2	G95018	hypothetical prote
116	3	8.8	31	2	G95022	hypothetical prote
117	3	8.8	31	2	A95085	hypothetical prote
118	3	8.8	31	2	H95093	hypothetical prote
119	3	8.8	31	2	E95151	hypothetical prote
120	3	8.8	31	2	E70202	hypothetical prote
121	3	8.8	31	2	E70223	hypothetical prote
122	3	8.8	31	2	H70225	hypothetical prote
123	3	8.8	31	2	C70240	hypothetical prote
124	3	8.8	31	2	H70252	hypothetical prote
125	3	8.8	31	2	S49191	hypothetical prote
126	3	8.8	31	2	H82353	hypothetical prote
127	3	8.8	31	2	B82151	hypothetical prote

128	3	8.8	31	2	A05051	hypothetical prote
129	3	8.8	31	2	B23605	histone H1.3 - whe
130	3	8.8	31	2	S78738	protein YOL038c-a
131	3	8.8	31	2	A36221	cecropin P1 - pig
132	3	8.8	31	2	S27112	sarcolipin - rabbi
133	3	8.8	31	2	C84082	hypothetical prote
134	3	8.8	31	2	D81591	hypothetical prote
135	3	8.8	31	2	G81558	hypothetical prote
136	3	8.8	31	2	G82816	hypothetical prote
137	3	8.8	31	2	F82565	hypothetical prote
138	3	8.8	31	2	C97398	hypothetical prote
139	3	8.8	32	1	TCEE	calcitonin - Japan
140	3	8.8	32	1	TCON2	calcitonin 2 - soc
141	3	8.8	32	1	TCON2C	calcitonin 2 - chu
142	3	8.8	32	1	TCON2P	calcitonin 2 - pin
143	3	8.8	32	1	TCON3	calcitonin 3 - coh
144	3	8.8	32	2	S20719	alcohol dehydrogen
145	3	8.8	32	2	A61143	trypsin (EC 3.4.21
146	3	8.8	32	2	D32502	T-cell receptor de
147	3	8.8	32	2	A32502	T-cell receptor de
148	3	8.8	32	2	B40186	ubiquitin / riboso
149	3	8.8	32	2	S57780	histone H3 - rice
150	3	8.8	32	2	A02687	DNA-binding protei
151	3	8.8	32	2	S51524	anchorin CII - bov
152	3	8.8	32	2	S36809	GTP-binding regula
153	3	8.8	32	2	A29743	translation initia
154	3	8.8	32	2	A03367	lectin - Macrotylo
155	3	8.8	32	2	A44900	fimbrin, SEF 21 -
156	3	8.8	32	2	S14300	zona pellucida-bin
157	3	8.8	32	2	S03273	photosystem II oxy
158	3	8.8	32	2	S08482	regulatory protein
159	3	8.8	32	2	E87694	hypothetical prote
160	3	8.8	32	2	D70222	hypothetical prote
161	3	8.8	32	2	E70225	hypothetical prote
162	3	8.8	32	2	B70241	hypothetical prote
163	3	8.8	32	2	B70257	hypothetical prote
164	3	8.8	32	2	D82353	hypothetical prote
165	3	8.8	32	2	E82279	hypothetical prote
166	3	8.8	32	2	E82089	hypothetical prote
167	3	8.8	32	2	H82416	hypothetical prote
168	3	8.8	32	2	T17394	vrlN protein - Dic
169	3	8.8	32	2	S23476	hypothetical prote
170	3	8.8	32	2	S22304	hypothetical prote
171	3	8.8	32	2	S78323	photosystem II pro
172	3	8.8	32	2	I38619	zinc finger protei
173	3	8.8	32	2	S28398	t-complex protein
174	3	8.8	32	2	T14569	hypothetical prote
175	3	8.8	32	2	H84081	hypothetical prote
176	3	8.8	32	2	F82833	hypothetical prote
177	3	8.8	32	2	JC5802	ovulation stimulat
178	3	8.8	32	2	E85588	hypothetical prote
179	3	8.8	33	2	S43312	2',3'-cyclic-nucle
180	3	8.8	33	2	S26859	chitinase (EC 3.2.
181	3	8.8	33	2	I52219	c-ras-Ki-2 protein
182	3	8.8	33	2	I53221	K-ras protein - hu
183	3	8.8	33	2	E32502	T-cell receptor de
184	3	8.8	33	2	A31461	T-cell receptor de

185	3	8.8	33	2	B31461	T-cell receptor de
186	3	8.8	33	2	S22604	ribosomal protein
187	3	8.8	33	2	A03150	retinoic acid-bind
188	3	8.8	33	2	C46027	neurotransmitter t
189	3	8.8	33	2	PQ0150	dnaK-type molecula
190	3	8.8	33	2	B44906	L1 protein - human
191	3	8.8	33	2	PQ0418	matrix protein M1
192	3	8.8	33	2	S34505	hypothetical prote
193	3	8.8	33	2	G95006	hypothetical prote
194	3	8.8	33	2	C95200	hypothetical prote
195	3	8.8	33	2	F84163	hypothetical prote
196	3	8.8	33	2	H82475	hypothetical prote
197	3	8.8	33	2	S68096	lactate dehydrogen
198	3	8.8	33	2	E82526	hypothetical prote
199	3	8.8	33	2	G85600	hypothetical prote
200	3	8.8	33	2	H85651	hypothetical prote
201	3	8.8	33	2	AC1012	hypothetical prote
202	3	8.8	33	2	C97406	hypothetical prote
203	3	8.8	34	2	S57282	phospholipase A2 (
204	3	8.8	34	2	A40298	dermaseptin - Sauv
205	3	8.8	34	2	JS0426	big gastrin - goat
206	3	8.8	34	2	I48887	cryptdin-4 - mouse
207	3	8.8	34	2	I32502	T-cell receptor de
208	3	8.8	34	2	H31461	T-cell receptor de
209	3	8.8	34	2	A19197	class II histocomp
210	3	8.8	34	2	D48147	troponin I (altern
211	3	8.8	34	2	A43564	neurogenic protein
212	3	8.8	34	2	H95047	hypothetical prote
213	3	8.8	34	2	D95189	hypothetical prote
214	3	8.8	34	2	C90973	hypothetical prote
215	3	8.8	34	2	F70242	hypothetical prote
216	3	8.8	34	2	B70252	hypothetical prote
217	3	8.8	34	2	F81919	hypothetical prote
218	3	8.8	34	2	F81044	hypothetical prote
219	3	8.8	34	2	F82163	hypothetical prote
220	3	8.8	34	2	E82100	hypothetical prote
221	3	8.8	34	2	B82449	hypothetical prote
222	3	8.8	34	2	S13662	cellulase (EC 3.2.
223	3	8.8	34	2	A60110	repetitive protein
224	3	8.8	34	2	S44828	F54F2.3 protein -
225	3	8.8	34	2	S40662	P-cadherin - mouse
226	3	8.8	34	2	F84079	hypothetical prote
227	3	8.8	34	2	H81600	hypothetical prote
228	3	8.8	34	2	H82820	hypothetical prote
229	3	8.8	34	2	C82819	hypothetical prote
230	3	8.8	34	2	C82764	hypothetical prote
231	3	8.8	34	2	B82679	hypothetical prote
232	3	8.8	34	2	G85820	unknown protein en
233	3	8.8	34	2	S12554	hydroxymethylgluta
234	3	8.8	35	2	JH0639	GTP-binding protei
235	3	8.8	35	2	S06667	toxin-like protein
236	3	8.8	35	2	E38601	Ig kappa chain V r
237	3	8.8	35	2	A05302	hemoglobin beta ch
238	3	8.8	35	2	S27154	ribosomal protein
239	3	8.8	35	2	S13435	lectin III - furze
240	3	8.8	35	2	S18224	filamentous hemagg
241	3	8.8	35	2	S18226	opacity protein op

242	3	8.8	35	2	T07870	major latex protei
243	3	8.8	35	2	B33770	hypothetical prote
244	3	8.8	35	2	PS0439	potassium channel
245	3	8.8	35	2	I48925	homeobox protein -
246	3	8.8	35	2	G95014	hypothetical prote
247	3	8.8	35	2	F87622	hypothetical prote
248	3	8.8	35	2	C96619	protein T30E16.7 [
249	3	8.8	35	2	B84674	hypothetical prote
250	3	8.8	35	2	F84395	hypothetical prote
251	3	8.8	35	2	B82012	hypothetical prote
252	3	8.8	35	2	H81948	hypothetical prote
253	3	8.8	35	2	A82151	hypothetical prote
254	3	8.8	35	2	F82051	hypothetical prote
255	3	8.8	35	2	I64003	hypothetical prote
256	3	8.8	35	2	F69827	hypothetical prote
257	3	8.8	35	2	C69977	hypothetical prote
258	3	8.8	35	2	A05057	hypothetical prote
259	3	8.8	35	2	S65772	early nodulin 40 -
260	3	8.8	35	2	G60529	hemocyanin M3' - c
261	3	8.8	35	2	S49309	oncofetal protein
262	3	8.8	35	2	C81560	hypothetical prote
263	3	8.8	35	2	B85708	unknown protein en
264	3	8.8	36	2	H32502	T-cell receptor de
265	3	8.8	36	2	C32502	T-cell receptor de
266	3	8.8	36	2	S08552	ribosomal protein
267	3	8.8	36	2	S72299	ribosomal protein
268	3	8.8	36	2	I46593	myosin - pig (frag
269	3	8.8	36	2	B31872	retinoic acid-bind
270	3	8.8	36	2	S35572	zona pellucida pro
271	3	8.8	36	2	B41481	virulence-associat
272	3	8.8	36	2	A38659	methanol dehydroge
273	3	8.8	36	2	E84416	hypothetical prote
274	3	8.8	36	2	S17834	acetyl-CoA carboxy
275	3	8.8	36	2	E70220	hypothetical prote
276	3	8.8	36	2	F70237	hypothetical prote
277	3	8.8	36	2	E70238	hypothetical prote
278	3	8.8	36	2	F64604	hypothetical prote
279	3	8.8	36	2	G81853	hypothetical prote
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281	3	8.8	36	2	G82281	hypothetical prote
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284	3	8.8	36	2	A82092	hypothetical prote
285	3	8.8	36	2	B82093	hypothetical prote
286	3	8.8	36	2	A82437	hypothetical prote
287	3	8.8	36	2	A69326	hypothetical prote
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289	3	8.8	36	2	T22263	hypothetical prote
290	3	8.8	36	2	A57443	guanylate cyclase
291	3	8.8	36	2	D83682	hypothetical prote
292	3	8.8	36	2	F84074	hypothetical prote
293	3	8.8	36	2	A56634	neuropeptide F - A
294	3	8.8	36	2	S77071	probable plastoqui
295	3	8.8	36	2	AF1015	hypothetical prote
296	3	8.8	36	2	AI1841	hypothetical prote
297	3	8.8	37	1	S32792	iberiotoxin - east
298	3	8.8	37	1	HSWT93	histone H2A.3 - wh

299	3	8.8	37	1	ZJBPF4	gene J protein - p
300	3	8.8	37	2	S48656	fusicoccin recepto
301	3	8.8	37	2	S03570	trypsin (EC 3.4.21
302	3	8.8	37	2	S39367	proteinase omega -
303	3	8.8	37	2	S06217	transforming prote
304	3	8.8	37	2	JH0735	Ig heavy chain V r
305	3	8.8	37	2	A30607	Ig kappa chain V-I
306	3	8.8	37	2	I48405	histone H2a - mous
307	3	8.8	37	2	B32307	ribosomal protein
308	3	8.8	37	2	S78257	ribosomal protein
309	3	8.8	37	2	AH1776	ribosomal protein
310	3	8.8	37	2	AI1400	ribosomal protein
311	3	8.8	37	2	E97282	ribosomal protein
312	3	8.8	37	2	F90019	50S ribosomal prot
313	3	8.8	37	2	PC1121	antifungal 25K pro
314	3	8.8	37	2	G01887	MEK kinase - human
315	3	8.8	37	2	S41509	probable antimutat
316	3	8.8	37	2	S07517	gene 6.3 protein -
317	3	8.8	37	2	E70241	hypothetical prote
318	3	8.8	37	2	D83199	hypothetical prote
319	3	8.8	37	2	H82304	hypothetical prote
320	3	8.8	37	2	S21132	photosystem II cyt
321	3	8.8	37	2	F59103	hypothetical prote
322	3	8.8	37	2	T36662	small hypothetical
323	3	8.8	37	2	T11815	hypothetical prote
324	3	8.8	37	2	A57127	diuretic hormone 1
325	3	8.8	37	2	C32112	R15 gamma peptide
326	3	8.8	37	2	G49050	T-cell surface gly
327	3	8.8	37	2	S68261	hypothetical prote
328	3	8.8	37	2	S49982	Tcell receptor alp
329	3	8.8	37	2	B39030	androgen-binding p
330	3	8.8	37	2	PN0550	metabotropic gluta
331	3	8.8	37	2	S70931	histone-like prote
332	3	8.8	37	2	F81403	hypothetical prote
333	3	8.8	38	1	R5EC36	ribosomal protein
334	3	8.8	38	2	C34047	stylar glycoprotei
335	3	8.8	38	2	T11763	acetyl-CoA carboxy
336	3	8.8	38	2	S39034	lipid transfer pro
337	3	8.8	38	2	PS0129	H-2 class I histoc
338	3	8.8	38	2	S50764	ribosomal protein
339	3	8.8	38	2	E72247	ribosomal protein
340	3	8.8	38	2	H83113	50S ribosomal prot
341	3	8.8	38	2	AG0028	50S ribosomal prot
342	3	8.8	38	2	D91149	50S ribosomal subu
343	3	8.8	38	2	AF1008	50S ribosomal chai
344	3	8.8	38	2	PH1920	annexin-like 40K p
345	3	8.8	38	2	S72344	pileE protein - Nei
346	3	8.8	38	2	JS0456	gene J protein - p
347	3	8.8	38	2	A60216	hyperglycemic horm
348	3	8.8	38	2	S65416	pyruvate synthase
349	3	8.8	38	2	H91111	hypothetical prote
350	3	8.8	38	2	D90631	hypothetical prote
351	3	8.8	38	2	E72306	hypothetical prote
352	3	8.8	38	2	E81873	hypothetical prote
353	3	8.8	38	2	T14885	hypothetical prote
354	3	8.8	38	2	A82478	hypothetical prote
355	3	8.8	38	2	E82463	hypothetical prote

356	3	8.8	38	2	A82450	hypothetical prote
357	3	8.8	38	2	G64001	hypothetical prote
358	3	8.8	38	2	D37842	hypothetical prote
359	3	8.8	38	2	B69492	hypothetical prote
360	3	8.8	38	2	S23173	photosystem I chai
361	3	8.8	38	2	S58601	hypothetical prote
362	3	8.8	38	2	T01741	hypothetical prote
363	3	8.8	38	2	B39888	synapsin I - bovin
364	3	8.8	38	2	B49012	orf 5' of megl - m
365	3	8.8	38	2	A83863	hypothetical prote
366	3	8.8	38	2	H81603	hypothetical prote
367	3	8.8	38	2	H81579	hypothetical prote
368	3	8.8	38	2	E82858	hypothetical prote
369	3	8.8	38	2	S71381	lebetin 2 isoform
370	3	8.8	38	2	G71305	probable ribosomal
371	3	8.8	38	2	B97327	hypothetical prote
372	3	8.8	38	2	H85994	50S ribosomal subu
373	3	8.8	38	2	T08652	hypothetical prote
374	3	8.8	38	2	T14226	NADH2 dehydrogenas
375	3	8.8	38	2	AH0774	hypothetical prote
376	3	8.8	39	1	CTDFAS	corticotropin - sp
377	3	8.8	39	1	HWGH3Z	exendin-3 - Mexica
378	3	8.8	39	1	HWGH4G	exendin-4 - Gila m
379	3	8.8	39	2	B45946	gamma-glutamyltran
380	3	8.8	39	2	S09645	hygromycin-B kinas
381	3	8.8	39	2	A01458	corticotropin - fi
382	3	8.8	39	2	PN0127	corticotropin - se
383	3	8.8	39	2	A61127	adrenocorticotropi
384	3	8.8	39	2	A01459	corticotropin - os
385	3	8.8	39	2	A01457	corticotropin - ra
386	3	8.8	39	2	C55995	prostaglandin E2 r
387	3	8.8	39	2	PH0878	Ig kappa chain V r
388	3	8.8	39	2	S72459	ribosomal protein
389	3	8.8	39	2	PQ0011	tubulin beta chain
390	3	8.8	39	2	S63482	tubulin beta chain
391	3	8.8	39	2	A45793	actin - nematode (
392	3	8.8	39	2	AH2286	photosystem II pro
393	3	8.8	39	2	G64944	yebJ protein - Esc
394	3	8.8	39	2	A85795	hypothetical prote
395	3	8.8	39	2	S78008	fucosyltransferase
396	3	8.8	39	2	H95146	hypothetical prote
397	3	8.8	39	2	D70239	hypothetical prote
398	3	8.8	39	2	C70254	hypothetical prote
399	3	8.8	39	2	G81899	hypothetical prote
400	3	8.8	39	2	B81912	hypothetical prote
401	3	8.8	39	2	B81954	very hypothetical
402	3	8.8	39	2	F82329	hypothetical prote
403	3	8.8	39	2	A44918	lactococcin G pept
404	3	8.8	39	2	S73118	photosystem II pro
405	3	8.8	39	2	PC4294	high mobility grou
406	3	8.8	39	2	T15158	hypothetical prote
407	3	8.8	39	2	I46466	luteinizing hormon
408	3	8.8	39	2	B40984	finger protein zfe
409	3	8.8	39	2	T03365	gene e2 protein -
410	3	8.8	39	2	F81587	hypothetical prote
411	3	8.8	39	2	E81540	hypothetical prote
412	3	8.8	39	2	C81745	hypothetical prote

413	3	8.8	39	2	T12905	hypothetical prote
414	3	8.8	39	2	D85739	hypothetical prote
415	3	8.8	39	2	AD0162	hypothetical prote
416	3	8.8	39	2	AE3109	hypothetical prote
417	3	8.8	40	1	SWFGS	sauvagine - Sauvag
418	3	8.8	40	2	B61320	plastocyanin - Aqu
419	3	8.8	40	2	S52343	hypothetical prote
420	3	8.8	40	2	S00264	creatine kinase (E
421	3	8.8	40	2	S34407	adenylate kinase (
422	3	8.8	40	2	S03688	type II site-speci
423	3	8.8	40	2	PQ0202	endo-1,4-beta-xyla
424	3	8.8	40	2	S50021	trypsin-like prote
425	3	8.8	40	2	B60908	beta-lactamase (EC
426	3	8.8	40	2	B41440	protein disulfide-
427	3	8.8	40	2	A19940	antithrombin III -
428	3	8.8	40	2	B59005	thymosin beta - sc
429	3	8.8	40	2	A59005	thymosin beta - se
430	3	8.8	40	2	B31791	sarcotoxin ID - fl
431	3	8.8	40	2	S07969	T-cell receptor al
432	3	8.8	40	2	I50012	MHC class I protei
433	3	8.8	40	2	I50013	MHC class I protei
434	3	8.8	40	2	S61539	ribosomal protein
435	3	8.8	40	2	A60171	proteoglycan core
436	3	8.8	40	2	A60645	tubulin beta chain
437	3	8.8	40	2	A29184	vitellogenin - tur
438	3	8.8	40	2	S65907	conglutin gamma -
439	3	8.8	40	2	S08656	protein VI - human
440	3	8.8	40	2	A53708	indolepyruvate syn
441	3	8.8	40	2	T08107	nonenzymatic prote
442	3	8.8	40	2	S71917	hemoglobin, extrac
443	3	8.8	40	2	S58853	homeotic protein u
444	3	8.8	40	2	H95063	hypothetical prote
445	3	8.8	40	2	H91281	hypothetical prote
446	3	8.8	40	2	A87642	hypothetical prote
447	3	8.8	40	2	F87419	hypothetical prote
448	3	8.8	40	2	C32338	hypothetical 4K pr
449	3	8.8	40	2	C72398	hypothetical prote
450	3	8.8	40	2	S44935	hypothetical prote
451	3	8.8	40	2	PC4218	hypothetical 40 pr
452	3	8.8	40	2	A82203	hypothetical prote
453	3	8.8	40	2	G82484	hypothetical prote
454	3	8.8	40	2	A82382	hypothetical prote
455	3	8.8	40	2	I39944	regulatory extrace
456	3	8.8	40	2	F69677	phosphatase (RapK)
457	3	8.8	40	2	I41476	probable antigen 9
458	3	8.8	40	2	S27709	hypothetical prote
459	3	8.8	40	2	T11811	hypothetical prote
460	3	8.8	40	2	T07472	hypothetical prote
461	3	8.8	40	2	T07516	hypothetical prote
462	3	8.8	40	2	T07523	hypothetical prote
463	3	8.8	40	2	T07560	hypothetical prote
464	3	8.8	40	2	T48629	hypothetical prote
465	3	8.8	40	2	S53001	mitotic-specific c
466	3	8.8	40	2	T03831	hypothetical prote
467	3	8.8	40	2	S56768	capsid protein - L
468	3	8.8	40	2	T07206	hypothetical prote
469	3	8.8	40	2	H81592	hypothetical prote

470	3	8.8	40	2	F81511	hypothetical prote
471	3	8.8	40	2	G82620	hypothetical prote
472	3	8.8	40	2	A82590	hypothetical prote
473	3	8.8	40	2	A86123	hypothetical prote
474	3	8.8	40	2	B97413	hypothetical prote
475	2	5.9	28	1	LFSEW	trp operon leader
476	2	5.9	28	1	LFEBLT	leu operon leader
477	2	5.9	28	1	LFECL	leu operon leader
478	2	5.9	28	1	G9BPSV	gene 9 protein - s
479	2	5.9	28	2	S41774	ubiquinol-cytochro
480	2	5.9	28	2	S71598	cytochrome P450 HP
481	2	5.9	28	2	S04341	cytochrome P450 PB
482	2	5.9	28	2	PX0033	cytochrome P450 te
483	2	5.9	28	2	S66436	allophycocyanin al
484	2	5.9	28	2	S47624	D-aspartate oxidas
485	2	5.9	28	2	T14210	NADH2 dehydrogenas
486	2	5.9	28	2	T14213	NADH2 dehydrogenas
487	2	5.9	28	2	T12301	NADH2 dehydrogenas
488	2	5.9	28	2	PC1162	cytochrome-c oxida
489	2	5.9	28	2	S21278	glutathione transf
490	2	5.9	28	2	C33948	glutathione transf
491	2	5.9	28	2	A34244	hexokinase (EC 2.7
492	2	5.9	28	2	D38578	protein kinase 4 (
493	2	5.9	28	2	B39116	epidermal growth f
494	2	5.9	28	2	A31859	deoxycytidine kina
495	2	5.9	28	2	B54257	deoxynucleoside ki
496	2	5.9	28	2	I55596	lysosomal acid lip
497	2	5.9	28	2	B35948	phospholipase A2 (
498	2	5.9	28	2	A35115	hypothetical prote
499	2	5.9	28	2	A61281	lysozyme homolog A
500	2	5.9	28	2	A61529	chymotrypsin (EC 3
501	2	5.9	28	2	A60291	24K proteinase (EC
502	2	5.9	28	2	S08186	proteasome beta ch
503	2	5.9	28	2	S55729	orotidine-5'-monop
504	2	5.9	28	2	I40034	trpE protein - Bac
505	2	5.9	28	2	A32643	deoxyribodipyrimid
506	2	5.9	28	2	S77854	glutamate-tRNA lig
507	2	5.9	28	2	JX0059	serine proteinase
508	2	5.9	28	2	S07156	trypsin inhibitor
509	2	5.9	28	2	JX0058	trypsin inhibitor
510	2	5.9	28	2	B45041	trypsin inhibitor
511	2	5.9	28	2	S20393	trypsin inhibitor
512	2	5.9	28	2	A25802	2S seed storage pr
513	2	5.9	28	2	T47196	RAS protein [impor
514	2	5.9	28	2	A61322	somatostatin-28 -
515	2	5.9	28	2	B60583	glycoprotein hormo
516	2	5.9	28	2	A38232	vasoactive intesti
517	2	5.9	28	2	A60303	vasoactive intesti
518	2	5.9	28	2	JT0412	bombyxin-IV chain
519	2	5.9	28	2	A56366	intestinal trefoil
520	2	5.9	28	2	C44180	alpha-neurotoxin-1
521	2	5.9	28	2	C39327	long neurotoxin -
522	2	5.9	28	2	I32529	Ig lambda chain V
523	2	5.9	28	2	PC1001	Ig light chain V r
524	2	5.9	28	2	B47719	T-cell receptor al
525	2	5.9	28	2	D47719	T-cell receptor al
526	2	5.9	28	2	S58389	T-cell receptor be

527	2	5.9	28	2	PH0250	T-cell receptor Vb
528	2	5.9	28	2	PH0247	T-cell receptor Vb
529	2	5.9	28	2	A49829	T-cell receptor va
530	2	5.9	28	2	D49829	T-cell receptor va
531	2	5.9	28	2	PH1908	T-cell receptor al
532	2	5.9	28	2	D41912	T-cell receptor be
533	2	5.9	28	2	G47719	house-dust-mite-re
534	2	5.9	28	2	E49533	T-cell receptor be
535	2	5.9	28	2	I46921	gene Bota protein
536	2	5.9	28	2	S11618	ribosomal protein
537	2	5.9	28	2	S51060	ribosomal protein
538	2	5.9	28	2	S51067	ribosomal protein
539	2	5.9	28	2	S72460	ribosomal protein
540	2	5.9	28	2	S08569	ribosomal protein
541	2	5.9	28	2	S55442	beta A2 crystallin
542	2	5.9	28	2	A45626	beta 2-tubulin - n
543	2	5.9	28	2	S21231	calcium-binding pr
544	2	5.9	28	2	A23691	apolipoprotein C-I
545	2	5.9	28	2	A05296	fibrinogen alpha c
546	2	5.9	28	2	A61113	cellular retinol-b
547	2	5.9	28	2	B35577	cell adhesion rece
548	2	5.9	28	2	I48349	fibronectin - mous
549	2	5.9	28	2	A61233	retinol-binding pr
550	2	5.9	28	2	I45911	dnaK-type molecula
551	2	5.9	28	2	PQ0263	dnaK-type molecula
552	2	5.9	28	2	A03356	omega-gliadin - ei
553	2	5.9	28	2	A60359	pollen allergen DG
554	2	5.9	28	2	PQ0691	photosystem I 5.6K
555	2	5.9	28	2	G32351	34K class B flagel
556	2	5.9	28	2	S47614	zinc finger protei
557	2	5.9	28	2	S49924	stp protein (Baker
558	2	5.9	28	2	PN0047	signal transductio
559	2	5.9	28	2	B39227	calcium channel pr
560	2	5.9	28	2	A36153	major allergen Ole
561	2	5.9	28	2	B54127	dolichyl-diphospho
562	2	5.9	28	2	S56746	alpha-synuclein, N
563	2	5.9	28	2	I48178	orphan receptor -
564	2	5.9	28	2	S29135	aminopyrine N-deme
565	2	5.9	28	2	S29136	aminopyrine N-deme
566	2	5.9	28	2	PN0625	homeobox JRX prote
567	2	5.9	28	2	B56779	tetM 5'-region lea
568	2	5.9	28	2	JU0297	fruR-shl operon le
569	2	5.9	28	2	G90638	leu operon leader
570	2	5.9	28	2	C90639	fruR leader peptid
571	2	5.9	28	2	B47310	MHVS28AA - murine
572	2	5.9	28	2	E64656	hypothetical prote
573	2	5.9	28	2	B64669	hypothetical prote
574	2	5.9	28	2	S15235	hypothetical prote
575	2	5.9	28	2	C56262	uvrB 3'-region hyp
576	2	5.9	28	2	E81239	hypothetical prote
577	2	5.9	28	2	I60364	phosphorybosylpyro
578	2	5.9	28	2	B39191	hypothetical prote
579	2	5.9	28	2	T17391	hypothetical prote
580	2	5.9	28	2	A56499	brevicin-27 - Lact
581	2	5.9	28	2	A41476	probable antigen 1
582	2	5.9	28	2	S16228	aryl acylamidase -
583	2	5.9	28	2	T37143	hypothetical prote

584	2	5.9	28	2	PS0106	2-phosphinomethylm
585	2	5.9	28	2	G69384	conserved hypothet
586	2	5.9	28	2	A69259	hypothetical prote
587	2	5.9	28	2	T06925	hypothetical prote
588	2	5.9	28	2	S38524	rRNA N-glycosidase
589	2	5.9	28	2	S21742	3-oxoacyl-[acyl-ca
590	2	5.9	28	2	PQ0800	calmodulin antagon
591	2	5.9	28	2	T06340	ribosomal protein
592	2	5.9	28	2	T07599	hypothetical prote
593	2	5.9	28	2	PH0220	peroxidase (EC 1.1
594	2	5.9	28	2	JQ0272	hypothetical 3K pr
595	2	5.9	28	2	S46250	fatty-acid-binding
596	2	5.9	28	2	A44923	carboxypeptidase 3
597	2	5.9	28	2	S64701	hypothetical prote
598	2	5.9	28	2	T38041	similarity to yeas
599	2	5.9	28	2	A60698	trichocyst protein
600	2	5.9	28	2	A27261	proteinase inhibit
601	2	5.9	28	2	A61417	bdellin B-3 - medi
602	2	5.9	28	2	S07826	venom protein - Am
603	2	5.9	28	2	C34923	omega-agatoxin IIA
604	2	5.9	28	2	A44877	cell surface prote
605	2	5.9	28	2	JW0019	mast cell degranul
606	2	5.9	28	2	A61273	interleukin-1 - st
607	2	5.9	28	2	S68643	nicotinic acetylch
608	2	5.9	28	2	PC2162	angiotensin II rec
609	2	5.9	28	2	I54183	cell adhesion regu
610	2	5.9	28	2	S54338	cytochrome P450 CY
611	2	5.9	28	2	I52627	erythrocyte chemok
612	2	5.9	28	2	JQ1035	hypothetical 3.2K
613	2	5.9	28	2	PH1335	Ig heavy chain DJ
614	2	5.9	28	2	PH1363	Ig heavy chain DJ
615	2	5.9	28	2	S37683	protein IEF SSP 91
616	2	5.9	28	2	S37686	protein IEF SSP 92
617	2	5.9	28	2	PH1911	T-cell receptor al
618	2	5.9	28	2	I39288	ZF3 domain - human
619	2	5.9	28	2	PL0005	pepsin A (EC 3.4.2
620	2	5.9	28	2	A60692	proline-rich prote
621	2	5.9	28	2	PC2239	heat shock protein
622	2	5.9	28	2	PT0366	T-cell receptor be
623	2	5.9	28	2	I58115	cystic fibrosis tr
624	2	5.9	28	2	A46690	sialic acid-specif
625	2	5.9	28	2	C83797	hypothetical prote
626	2	5.9	28	2	C83969	hypothetical prote
627	2	5.9	28	2	S51593	myrB protein - Mic
628	2	5.9	28	2	C85490	fruR leader peptid
629	2	5.9	28	2	C97078	hypothetical prote
630	2	5.9	28	2	F97000	hypothetical prote
631	2	5.9	28	2	G85489	leu operon leader
632	2	5.9	28	2	AB1093	hypothetical prote
633	2	5.9	28	2	T06490	probable ribulose-
634	2	5.9	28	2	AG0516	leu operon leader
635	2	5.9	28	4	I68614	frame shifted FMR1
636	2	5.9	28	4	JN0014	GABA(A) receptor a
637	2	5.9	29	1	TIPU	trypsin inhibitor
638	2	5.9	29	1	TIPU3	trypsin inhibitor
639	2	5.9	29	1	TIPU2B	trypsin inhibitor
640	2	5.9	29	1	GCOPV	glucagon - North A

641	2	5.9	29	1	GCDK	glucagon - duck
642	2	5.9	29	1	A61583	glucagon - ostrich
643	2	5.9	29	1	GCFLE	glucagon - Europea
644	2	5.9	29	1	GCDF	glucagon - smaller
645	2	5.9	29	1	GCEN	glucagon - elephan
646	2	5.9	29	1	GCTTS	glucagon - slider
647	2	5.9	29	1	TNLJBR	trans-activating t
648	2	5.9	29	1	Q1BP57	gene 1.5 protein -
649	2	5.9	29	2	A60558	cytochrome P450 HL
650	2	5.9	29	2	T17079	NADH2 dehydrogenas
651	2	5.9	29	2	A48427	flavohemoglobin hm
652	2	5.9	29	2	A54234	cytochrome-c oxida
653	2	5.9	29	2	S08201	peroxidase (EC 1.1
654	2	5.9	29	2	A26208	acetyl-CoA C-acety
655	2	5.9	29	2	A22018	phosphotransferase
656	2	5.9	29	2	S46211	kallikrein rK8 (pK
657	2	5.9	29	2	S28174	heat-shock protein
658	2	5.9	29	2	A32414	bothrolysin (EC 3.
659	2	5.9	29	2	S17432	H+-transporting tw
660	2	5.9	29	2	S02578	H+-transporting tw
661	2	5.9	29	2	S23122	peptidylprolyl iso
662	2	5.9	29	2	JU0211	squash-type trypsi
663	2	5.9	29	2	T03653	phospholipid trans
664	2	5.9	29	2	C24536	alpha-amylase/tryp
665	2	5.9	29	2	C25310	alpha-amylase/tryp
666	2	5.9	29	2	D55998	brevinin-2Ed - edi
667	2	5.9	29	2	D53578	brevinin-2Ee - edi
668	2	5.9	29	2	A61509	islet amyloid poly
669	2	5.9	29	2	A91740	glucagon - turkey
670	2	5.9	29	2	A91741	glucagon - rabbit
671	2	5.9	29	2	A91742	glucagon - Arabian
672	2	5.9	29	2	S07211	glucagon - marbled
673	2	5.9	29	2	A61135	glucagon - bigeye
674	2	5.9	29	2	C39258	glucagon - common
675	2	5.9	29	2	C60840	glucagon I - Europ
676	2	5.9	29	2	S39018	glucagon - bowfin
677	2	5.9	29	2	A39462	cholestokinin - do
678	2	5.9	29	2	A60791	toxin II.9 - scorp
679	2	5.9	29	2	A43620	omega-conotoxin GV
680	2	5.9	29	2	B43620	omega-conotoxin GV
681	2	5.9	29	2	A58537	omega-conotoxin MV
682	2	5.9	29	2	I52628	low affinity nerve
683	2	5.9	29	2	C61233	conceptus protein
684	2	5.9	29	2	S10061	Ig heavy chain (cl
685	2	5.9	29	2	PH1328	Ig heavy chain DJ
686	2	5.9	29	2	PH0239	T-cell receptor Vb
687	2	5.9	29	2	PH0251	T-cell receptor Vb
688	2	5.9	29	2	PH0254	T-cell receptor Vb
689	2	5.9	29	2	PH0233	T-cell receptor Vb
690	2	5.9	29	2	E31485	Ig heavy chain V r
691	2	5.9	29	2	H31485	Ig kappa chain V r
692	2	5.9	29	2	G31461	T-cell receptor de
693	2	5.9	29	2	C47719	T-cell receptor al
694	2	5.9	29	2	E47719	house-dust-mite-re
695	2	5.9	29	2	PS0134	H-2 class I histoc
696	2	5.9	29	2	PS0132	H-2 class I histoc
697	2	5.9	29	2	D32533	class II histocomp

698	2	5.9	29	2	I37534	gene HLA-DRB prote
699	2	5.9	29	2	I37535	gene HLA-DRB prote
700	2	5.9	29	2	I37536	MHC class II histo
701	2	5.9	29	2	I37301	MHC class II histo
702	2	5.9	29	2	I37303	HLA-DR beta - huma
703	2	5.9	29	2	I37306	HLA-DR beta - huma
704	2	5.9	29	2	I50214	protein-tyrosine-p
705	2	5.9	29	2	S07771	histone H2B.2, spe
706	2	5.9	29	2	T04412	histone H3 - barle
707	2	5.9	29	2	S51070	ribosomal protein
708	2	5.9	29	2	S08555	ribosomal protein
709	2	5.9	29	2	PC4231	ribosomal protein
710	2	5.9	29	2	S10050	ribosomal protein
711	2	5.9	29	2	S10049	ribosomal protein
712	2	5.9	29	2	S26229	ribosomal protein
713	2	5.9	29	2	A27561	ribosomal protein
714	2	5.9	29	2	S10725	Meth A tumor-speci
715	2	5.9	29	2	E33208	calmodulin-binding
716	2	5.9	29	2	C33208	calreticulin, uter
717	2	5.9	29	2	D33208	calreticulin, slow
718	2	5.9	29	2	A45474	calreticulin, brai
719	2	5.9	29	2	G39690	thrombospondin 2 -
720	2	5.9	29	2	A61166	neural cell adhesi
721	2	5.9	29	2	I52402	endometrial proges
722	2	5.9	29	2	S00564	alpha-fetoprotein
723	2	5.9	29	2	S57232	enamel protein - r
724	2	5.9	29	2	A43038	homeotic protein s
725	2	5.9	29	2	T12082	auxin-binding prot
726	2	5.9	29	2	S70328	proline-rich prote
727	2	5.9	29	2	S29208	gamma35 secalin -
728	2	5.9	29	2	S07055	avenin gamma-3 - o
729	2	5.9	29	2	S05032	photosystem I prot
730	2	5.9	29	2	S08088	photosystem II pro
731	2	5.9	29	2	F42075	gene VII protein -
732	2	5.9	29	2	T51116	finger protein (cl
733	2	5.9	29	2	A53145	probable precorrin
734	2	5.9	29	2	A35121	high conductance c
735	2	5.9	29	2	S03277	hypothetical prote
736	2	5.9	29	2	S63509	photosystem II 5K
737	2	5.9	29	2	A55891	glycine reductase
738	2	5.9	29	2	S32730	delta-conotoxin Gm
739	2	5.9	29	2	S57225	homeotic protein -
740	2	5.9	29	2	S32732	labial protein (cl
741	2	5.9	29	2	S32734	homeotic protein -
742	2	5.9	29	2	S32733	homeotic protein -
743	2	5.9	29	2	S07513	homeotic protein -
744	2	5.9	29	2	S14040	gene 5.1 protein -
745	2	5.9	29	2	E64586	hypothetical prote
746	2	5.9	29	2	B64607	hypothetical prote
747	2	5.9	29	2	G83440	hypothetical prote
748	2	5.9	29	2	A49288	KdpF protein PA163
749	2	5.9	29	2	B81136	alcohol dehydrogen
750	2	5.9	29	2	A81078	hypothetical prote
751	2	5.9	29	2	B81006	hypothetical prote
752	2	5.9	29	2	A35445	hypothetical prote
753	2	5.9	29	2	S19943	repY protein - Esc
754	2	5.9	29	2	A49914	aadB protein - Kle
						S-layer protein va

755	2	5.9	29	2	E64036	hypothetical prote
756	2	5.9	29	2	B48363	2-hydroxyglutaryl-
757	2	5.9	29	2	C40638	orf 3' of cycI - R
758	2	5.9	29	2	S05224	photosystem I 4.8K
759	2	5.9	29	2	B56817	photosystem I chai
760	2	5.9	29	2	S74572	hypothetical prote
761	2	5.9	29	2	C60743	putrescine carbamo
762	2	5.9	29	2	S67989	HA-19/HA-52 protei
763	2	5.9	29	2	S14099	12-alpha-hydroxyst
764	2	5.9	29	2	S77569	plantaricin SA6 -
765	2	5.9	29	2	S21222	48K protein - Euba
766	2	5.9	29	2	S03947	hydrogen dehydroge
767	2	5.9	29	2	T34643	hypothetical prote
768	2	5.9	29	2	T37120	hypothetical prote
769	2	5.9	29	2	T36654	probable small mem
770	2	5.9	29	2	B43937	endo-1,4-beta-xyla
771	2	5.9	29	2	S09556	hypothetical prote
772	2	5.9	29	2	T06904	hypothetical prote
773	2	5.9	29	2	S73197	hypothetical prote
774	2	5.9	29	2	S78326	conserved hypothet
775	2	5.9	29	2	S78310	hypothetical prote
776	2	5.9	29	2	S78360	hypothetical prote
777	2	5.9	29	2	S01572	hypothetical prote
778	2	5.9	29	2	T07450	hypothetical prote
779	2	5.9	29	2	S01448	hypothetical prote
780	2	5.9	29	2	S38525	rRNA N-glycosidase
781	2	5.9	29	2	T52557	translation elonga
782	2	5.9	29	2	PQ0862	allantoinase (EC 3
783	2	5.9	29	2	PQ0486	globulin 2a - taro
784	2	5.9	29	2	S02200	prolamin alpha-1 -
785	2	5.9	29	2	A60683	malate dehydrogena
786	2	5.9	29	2	JQ0212	hypothetical 3K pr
787	2	5.9	29	2	S58541	hypothetical prote
788	2	5.9	29	2	PC2035	alanine transamina
789	2	5.9	29	2	S78714	protein YDR524w-a
790	2	5.9	29	2	S68094	2,3-dihydroxybenzo
791	2	5.9	29	2	B21112	variant surface gl
792	2	5.9	29	2	C60110	repetitive protein
793	2	5.9	29	2	D24802	cuticle protein 36
794	2	5.9	29	2	A56591	E75 steroid recept
795	2	5.9	29	2	A61613	ceratotoxin A - Me
796	2	5.9	29	2	B61613	ceratotoxin B - Me
797	2	5.9	29	2	PH1230	lectin - namazu (f
798	2	5.9	29	2	A32860	biotin-binding pro
799	2	5.9	29	2	I50382	c-mil protein - ch
800	2	5.9	29	2	I50695	non-collagenous al
801	2	5.9	29	2	B54197	70k thyroid autoan
802	2	5.9	29	2	A35891	carcinoembryonic a
803	2	5.9	29	2	I77372	CD44SP - human
804	2	5.9	29	2	S54340	diazepam binding i
805	2	5.9	29	2	A41683	hyaluronate recept
806	2	5.9	29	2	C54037	splicing regulator
807	2	5.9	29	2	S35924	T-cell receptor ga
808	2	5.9	29	2	A60604	glutathione peroxi
809	2	5.9	29	2	A27688	mammary-derived gr
810	2	5.9	29	2	S57204	oviduct-specific s
811	2	5.9	29	2	I47025	antigen WC1 [impor

812	2	5.9	29	2	A49410	t-complex polypept
813	2	5.9	29	2	PS0125	H-2 class I histoc
814	2	5.9	29	2	S46929	teg169 protein - m
815	2	5.9	29	2	S38749	vimentin homolog -
816	2	5.9	29	2	S42764	Ca2+/calmodulin-de
817	2	5.9	29	2	A49708	synaptosomal-assoc
818	2	5.9	29	2	H83777	hypothetical prote
819	2	5.9	29	2	C83833	hypothetical prote
820	2	5.9	29	2	F83870	hypothetical prote
821	2	5.9	29	2	B84144	hypothetical prote
822	2	5.9	29	2	PC4421	multactivase (EC 3
823	2	5.9	29	2	B85840	hypothetical prote
824	2	5.9	29	2	C85840	hypothetical prote
825	2	5.9	29	2	G86058	hypothetical prote
826	2	5.9	29	2	E89904	hypothetical prote
827	2	5.9	29	2	H89949	hypothetical prote
828	2	5.9	29	2	S17496	inorganic diphosph
829	2	5.9	29	2	PQ0782	NADH2 dehydrogenas
830	2	5.9	29	2	S34762	L-serine ammonia-l
831	2	5.9	29	2	AB0717	hypothetical prote
832	2	5.9	29	2	AC0717	hypothetical prote
833	2	5.9	29	2	AH2338	PetN protein [impo
834	2	5.9	29	4	I58970	hypothetical prote
835	2	5.9	30	1	AIBSAF	thermophilic amino
836	2	5.9	30	1	TIPU1W	trypsin inhibitor
837	2	5.9	30	1	OEON2K	beta-endorphin II
838	2	5.9	30	1	IRTRC3	protamine CIII, ma
839	2	5.9	30	1	IRTRC2	protamine Ia - rai
840	2	5.9	30	1	IRTR78	protamine CIII, mi
841	2	5.9	30	1	IRTR4	protamine pTP4 - r
842	2	5.9	30	1	CLHRY2	protamine YII - Pa
843	2	5.9	30	1	CLHR2A	protamine YII - At
844	2	5.9	30	1	SNUMP	sillucin - Rhizomu
845	2	5.9	30	2	I57689	ubiquinol-cytochro
846	2	5.9	30	2	I52254	gene CYP11B2 prote
847	2	5.9	30	2	B56859	fatty acid omega-h
848	2	5.9	30	2	A27375	photosystem I iron
849	2	5.9	30	2	S11131	NADH2 dehydrogenas
850	2	5.9	30	2	S14214	NADH2 dehydrogenas
851	2	5.9	30	2	PQ0723	parvalbumin [impor
852	2	5.9	30	2	S08202	peroxidase (EC 1.1
853	2	5.9	30	2	S08204	peroxidase (EC 1.1
854	2	5.9	30	2	S08203	peroxidase (EC 1.1
855	2	5.9	30	2	A39089	hydrogenase (EC 1.
856	2	5.9	30	2	I38066	nitric-oxide synth
857	2	5.9	30	2	I39799	CAT-66 - Bacillus
858	2	5.9	30	2	A18780	dimethylallyltrans
859	2	5.9	30	2	S03283	methionine adenosy
860	2	5.9	30	2	A28562	glutathione transf
861	2	5.9	30	2	B27103	aspartate transami
862	2	5.9	30	2	A27103	aspartate transami
863	2	5.9	30	2	I55427	aspartate transami
864	2	5.9	30	2	A49955	protein-tyrosine k
865	2	5.9	30	2	S68639	nigroxin A - black
866	2	5.9	30	2	S68640	nigroxin B - black
867	2	5.9	30	2	S15678	acetylcholinestera
868	2	5.9	30	2	A05004	pancreatic ribonuc

869	2	5.9	30	2	A44598	endo-1,4-beta-xyla
870	2	5.9	30	2	PC2361	alpha-glucosidase
871	2	5.9	30	2	PX0073	epoxide hydrolase
872	2	5.9	30	2	B60291	30K serine protein
873	2	5.9	30	2	A27634	major fecal allerg
874	2	5.9	30	2	B27634	major fecal allerg
875	2	5.9	30	2	I77411	renin-2 - mouse (f
876	2	5.9	30	2	PC2328	proteasome endopep
877	2	5.9	30	2	A34486	inorganic diphosph
878	2	5.9	30	2	S21816	H+-exporting ATPas
879	2	5.9	30	2	S21814	H+-exporting ATPas
880	2	5.9	30	2	S74121	fructose-bisphosph
881	2	5.9	30	2	S25666	phosphopyruvate hy
882	2	5.9	30	2	S69600	peptidylprolyl iso
883	2	5.9	30	2	A60517	alpha-1-antitrypsi
884	2	5.9	30	2	S24979	proteinase inhibit
885	2	5.9	30	2	JX0057	trypsin inhibitor
886	2	5.9	30	2	JS0579	squash-type trypsi
887	2	5.9	30	2	JQ1958	trypsin inhibitor
888	2	5.9	30	2	PC1113	proteinase inhibit
889	2	5.9	30	2	C42842	antifungal 2S stor
890	2	5.9	30	2	S70341	napin large chain
891	2	5.9	30	2	S70343	napin large chain
892	2	5.9	30	2	A33308	thrombomodulin - r
893	2	5.9	30	2	S01657	atrial natriuretic
894	2	5.9	30	2	A61130	somatotropin - Ame
895	2	5.9	30	2	S44473	glucagon-like pept
896	2	5.9	30	2	A59076	defensin alpha-1 -
897	2	5.9	30	2	B59076	defensin alpha-2 -
898	2	5.9	30	2	C59076	defensin alpha-3 -
899	2	5.9	30	2	B60791	toxin II.6 - scorp
900	2	5.9	30	2	A31187	neurotoxin II.22.5
901	2	5.9	30	2	I68109	interferon alpha-W
902	2	5.9	30	2	C49533	T-cell receptor al
903	2	5.9	30	2	S20778	Ig heavy chain V r
904	2	5.9	30	2	PL0092	Ig heavy chain V r
905	2	5.9	30	2	PH0245	T-cell receptor Vb
906	2	5.9	30	2	PH0228	T-cell receptor Vb
907	2	5.9	30	2	PH0252	T-cell receptor Vb
908	2	5.9	30	2	PH0882	Ig kappa chain V r
909	2	5.9	30	2	E31461	T-cell receptor de
910	2	5.9	30	2	PH0235	T-cell receptor Vb
911	2	5.9	30	2	A49533	T-cell receptor al
912	2	5.9	30	2	C27579	T-cell receptor be
913	2	5.9	30	2	I37626	Fc gamma (IgG) rec
914	2	5.9	30	2	PS0121	H-2 class I histoc
915	2	5.9	30	2	S74192	crotoxin inhibitor
916	2	5.9	30	2	A05253	hemoglobin epsilon
917	2	5.9	30	2	A21680	hemoglobin epsilon
918	2	5.9	30	2	A05254	hemoglobin epsilon
919	2	5.9	30	2	S68618	histone H2B - sea
920	2	5.9	30	2	PD0014	cAMP response elem
921	2	5.9	30	2	PN0651	restriction endonu
922	2	5.9	30	2	S11613	ribosomal protein
923	2	5.9	30	2	B29164	cartilage proteogl
924	2	5.9	30	2	A60511	gamma-crystallin -
925	2	5.9	30	2	I49412	gamma-crystallin-3

926	2	5.9	30	2	S12965	gamma-crystallin -
927	2	5.9	30	2	S69269	ezrin homolog - bo
928	2	5.9	30	2	A61189	tubulin beta chain
929	2	5.9	30	2	I52806	Duchenne muscular
930	2	5.9	30	2	S21153	calcium-binding pr
931	2	5.9	30	2	A26188	lipocortin I - pig
932	2	5.9	30	2	A56790	annexin, isoform P
933	2	5.9	30	2	A34622	fibrinogen beta ch
934	2	5.9	30	2	A03148	retinol-binding pr
935	2	5.9	30	2	A48299	taurine transporte
936	2	5.9	30	2	B61511	serum albumin, mil
937	2	5.9	30	2	B39819	neutrophil chemota
938	2	5.9	30	2	A38933	vitronectin - bovi
939	2	5.9	30	2	S57234	fushi tarazu segme
940	2	5.9	30	2	S69124	rRNA N-glycosidase
941	2	5.9	30	2	S69125	rRNA N-glycosidase
942	2	5.9	30	2	S07065	rRNA N-glycosidase
943	2	5.9	30	2	A31836	17K antigen - Rick
944	2	5.9	30	2	PQ0669	photosystem I 17.5
945	2	5.9	30	2	E45095	photosystem I ligh
946	2	5.9	30	2	B45095	photosystem I ligh
947	2	5.9	30	2	A44913	34K core flagella
948	2	5.9	30	2	B24987	regulatory protein
949	2	5.9	30	2	S30757	genome polyprotein
950	2	5.9	30	2	S30760	genome polyprotein
951	2	5.9	30	2	S30759	genome polyprotein
952	2	5.9	30	2	B44314	intracisternal A p
953	2	5.9	30	2	S13753	replication initia
954	2	5.9	30	2	S26175	tail tubular prote
955	2	5.9	30	2	S69352	N-methylhydantoin
956	2	5.9	30	2	S68312	glucuronosyltransf
957	2	5.9	30	2	PH1228	D-aminoacylase (EC
958	2	5.9	30	2	S42364	aromatic-amino-aci
959	2	5.9	30	2	S05223	photosystem I 6.5K
960	2	5.9	30	2	S28991	antifungal protein
961	2	5.9	30	2	PC2307	X-Pro aminopeptida
962	2	5.9	30	2	PQ0484	globulin lb - taro
963	2	5.9	30	2	C43591	51K outer membrane
964	2	5.9	30	2	B43591	45K outer membrane
965	2	5.9	30	2	S06411	killer plasmid 28K
966	2	5.9	30	2	B49292	GDP dissociation i
967	2	5.9	30	2	A60914	pheromone-binding
968	2	5.9	30	2	PS0437	potassium channel
969	2	5.9	30	2	PS0438	potassium channel
970	2	5.9	30	2	A47607	immunogenic protei
971	2	5.9	30	2	S02088	blood group Rh-rel
972	2	5.9	30	2	S29138	aniline monooxygen
973	2	5.9	30	2	S57227	proboscipedia prot
974	2	5.9	30	2	H95008	hypothetical prote
975	2	5.9	30	2	C95030	hypothetical prote
976	2	5.9	30	2	G95031	hypothetical prote
977	2	5.9	30	2	E95079	hypothetical prote
978	2	5.9	30	2	F95118	hypothetical prote
979	2	5.9	30	2	E95145	hypothetical prote
980	2	5.9	30	2	F89406	protein R10E8.7 [i
981	2	5.9	30	2	F87254	hypothetical prote
982	2	5.9	30	2	E84786	hypothetical prote

983	2	5.9	30	2	C84481	hypothetical prote
984	2	5.9	30	2	B47483	cysteine-rich para
985	2	5.9	30	2	S15141	hypothetical prote
986	2	5.9	30	2	S13985	hypothetical prote
987	2	5.9	30	2	S14038	hypothetical prote
988	2	5.9	30	2	S13994	hypothetical prote
989	2	5.9	30	2	A72205	hypothetical prote
990	2	5.9	30	2	E72356	hypothetical prote
991	2	5.9	30	2	H72312	hypothetical prote
992	2	5.9	30	2	S66448	trimethylamine deh
993	2	5.9	30	2	A70105	conserved hypothet
994	2	5.9	30	2	F70118	hypothetical prote
995	2	5.9	30	2	D70144	hypothetical prote
996	2	5.9	30	2	H70152	hypothetical prote
997	2	5.9	30	2	A70209	hypothetical prote
998	2	5.9	30	2	E70246	hypothetical prote
999	2	5.9	30	2	F70253	hypothetical prote
1000	2	5.9	30	2	F70254	hypothetical prote

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 14.7%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28

|||||

Db 26 LRKKL 30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 14.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5

|||||

Db 30 SVSEI 34

RESULT 3

E95098

hypothetical protein SP0853 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:
A;Gene: SP0853

Query Match 14.7%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 4

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 11.8%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 5

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.; Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.

J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 6

S01614

dystrophin - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: S01614

R;Nudel, U.; Robzyk, K.; Yaffe, D.

Nature 331, 635-638, 1988

A;Title: Expression of the putative Duchenne muscular dystrophy gene in differentiated myogenic cell cultures and in the brain.

A;Reference number: S01614; MUID:88122671; PMID:3340214

A;Accession: S01614

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-29 <NUD>

A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214

C;Genetics:

A;Map position: X

C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology; WW repeat homology

C;Keywords: actin binding; cytoskeleton

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 7

I78537

copper transporting P-type ATPase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I78537

R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 8

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10,'XXP',14-15,'X',17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 9

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.
Eur. J. Biochem. 233, 800-808, 1995

A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate
dehydrogenase genes from the thermophilic archaeon *Sulfolobus solfataricus*
overlap by 8-bp: isolation, sequencing of the genes and expression in
Escherichia coli.

A;Reference number: S63528; MUID:96085144; PMID:8521845

A;Accession: S63531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-30 <JON>

A;Cross-references: EMBL:X80178

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26

||||

Db 11 WLRK 14

RESULT 10

S44471

glucagon G1 - North American paddlefish (*Polyodon spathula*)

C;Species: *Polyodon spathula*

C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999

C;Accession: S44471

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a
phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44471

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Experimental source: pancreas

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24

||||

Db 23 VEWL 26

RESULT 11

S44472

glucagon G2 - North American paddlefish (*Polyodon spathula*)

C;Species: *Polyodon spathula*

C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999

C;Accession: S44472

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
 ||||
Db 23 VEWL 26

RESULT 12

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058; TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 26 KKLQ 29

RESULT 13

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 14

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
|||
Db 8 MERV 11

RESULT 15

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84161
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
 Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.;
 Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,
 R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;
 Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,
 J.L.; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,
 T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: G84161
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-32 <STO>
 A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG0019H

Query Match 11.8%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 16

E81714
 hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
 C;Accession: E81714
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
 Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
 Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
 W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
 C.M.
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
 AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: E81714
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-33 <TET>
 A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;
 PID:g7190379; GSPDB:GN00121; TIGR:TC0337
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0337

Query Match 11.8%; Score 4; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
Db 26 LRKK 29

RESULT 17

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
Db 29 SVSE 32

RESULT 18

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
Db 29 SVSE 32

RESULT 19

D82125

hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 24 KKLQ 27

RESULT 20

S70806

hypothetical protein 5 - *Vibrio cholerae* (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: *Vibrio cholerae*

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20
 ||||
 Db 14 SMER 17

RESULT 21

F95057

hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.;

Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0497

Query Match 11.8%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 10 KKLQ 13

RESULT 22

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 4 KKLQ 7

RESULT 23

S46227

hypothetical protein - *Streptomyces chrysomallus* (fragment)

C;Species: *Streptomyces chrysomallus*

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: *Streptomyces chrysomallus* FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 27 ERVE 30

RESULT 24

S71912

hemoglobin, extracellular, chain A1 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 25 ERVE 28

RESULT 25

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
 ||||
Db 6 RKKL 9

RESULT 26

A43933

antigen 5 epitope - tapeworm (*Echinococcus granulosus*) (fragment)

C;Species: *Echinococcus granulosus*

C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

C;Accession: A43933

R;Chamekh, M.; Gras-Masse, H.; Bossus, M.; Facon, B.; Dissous, C.; Tartar, A.; Capron, A.

J. Clin. Invest. 89, 458-464, 1992

A;Title: Diagnostic value of a synthetic peptide derived from Echinococcus granulosus recombinant protein.

A;Reference number: A43933; MUID:92147859; PMID:1737836

A;Accession: A43933

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: GB:M74034

A;Note: sequence extracted from NCBI backbone (NCBIP:81239)

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKGK 13
 ||||
Db 10 NKGK 13

RESULT 27

CKFHCS

sarcotoxin IC - flesh fly (Sarcophaga peregrina)

C;Species: Sarcophaga peregrina

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997

A;Accession: C22625

A;Molecule type: protein

A;Residues: 1-39 <OKA>

C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial; hemolymph

F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
Db 2 WLRK 5

RESULT 28

S71913

hemoglobin, extracellular, chain A2 - polychaete (Perinereis aibuhitensis) (fragment)

C;Species: Perinereis aibuhitensis

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.
Biochim. Biophys. Acta 1290, 215-223, 1996
A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.
A;Reference number: S71912; MUID:96350431; PMID:8765123
A;Accession: S71913
A;Molecule type: protein
A;Residues: 1-39 <MAT>
C;Superfamily: globin; globin homology
C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 27 ERVE 30

RESULT 29

S77164

ycf32 protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sml0007

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S77164

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77164

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-39 <KAN>

A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17722.1; PID:g1652803

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: ycf32

C;Superfamily: hypothetical protein ycf32

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
 ||||
Db 31 LQDV 34

RESULT 30

A42272

brain-type creatine kinase, peptide, B - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, Squalus acanthias.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28

|||

Db 10 KKL 12

RESULT 31

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake (fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7

|||

Db 3 IQL 5

RESULT 32

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 33

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 34

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999
 C;Accession: S58386
 R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.
 Nucleic Acids Res. 23, 3074-3075, 1995
 A;Title: A novel method for sequencing members of multi-gene families.
 A;Reference number: S58384; MUID:95388532; PMID:7659534
 A;Accession: S58386
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-28 <JOH>
 A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 A;Note: only a part of the coding sequence is given
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 12 ERV 14

RESULT 35

S10052
 ribosomal protein L37.e - fission yeast (Schizosaccharomyces pombe) (fragment)
 N;Alternate names: ribosomal protein SP-L27
 C;Species: Schizosaccharomyces pombe
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-Sep-1993
 C;Accession: S10052
 R;Otaka, E.; Higo, K.I.; Itoh, T.
 Mol. Gen. Genet. 191, 519-524, 1983
 A;Title: Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from Schizosaccharomyces pombe.
 A;Reference number: S07293; MUID:84038947; PMID:6355773
 A;Accession: S10052
 A;Molecule type: protein
 A;Residues: 1-28 <OTA>
 C;Superfamily: rat ribosomal protein L37
 C;Keywords: protein biosynthesis; ribosome

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
 |||
 Db 21 KGK 23

RESULT 36

A60752

outer membrane protein A - *Yersinia pseudotuberculosis* (fragment)
 N;Alternate names: heat-modifiable protein; outer membrane protein II
 C;Species: *Yersinia pseudotuberculosis*
 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 17-Mar-1999
 C;Accession: A60752
 R;Zhang, J.J.; Hamachi, M.; Hamachi, T.; Zhao, Y.P.; Yu, D.T.Y.
 J. Immunol. 143, 2955-2960, 1989
 A;Title: The bacterial outer membrane protein that reacts with anti-HLA-B27
 antibodies is the OmpA protein.
 A;Reference number: A60752; MUID:90038529; PMID:2478630
 A;Accession: A60752
 A;Molecule type: protein
 A;Residues: 1-28 <ZHA>
 C;Genetics:
 A;Gene: ompA
 C;Superfamily: outer membrane protein A
 C;Keywords: membrane protein

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKG 12
 |||
 Db 26 NKG 28

RESULT 37

S56121

type I DNA methyltransferase M.EcoR124I chain HsdS - *Escherichia coli*
 (fragments)

C;Species: *Escherichia coli*
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
 C;Accession: S56121
 R;Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.
 J. Mol. Biol. 250, 181-190, 1995
 A;Title: Probing the domain structure of the type IC DNA methyltransferase
 M.EcoR124I by limited proteolysis.
 A;Reference number: S56121; MUID:95333175; PMID:7608969
 A;Accession: S56121
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-28 <WEB>

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 DVH 32
 |||
 Db 8 DVH 10

RESULT 38

S70894

hypothetical protein 1 - *Vibrio anguillarum* (fragment)
 C;Species: *Vibrio anguillarum*

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S70894
R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
Mol. Microbiol. 19, 625-637, 1996
A;Title: Chemotactic motility is required for invasion of the host by the fish
pathogen *Vibrio anguillarum*.
A;Reference number: S70894; MUID:96228710; PMID:8830252
A;Accession: S70894
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <OTO>
A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1;
PID:g1723992

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
|||
Db 18 LNS 20

RESULT 39

S22469

hypothetical protein 1 - *Prochlorothrix hollandica*

C;Species: *Prochlorothrix hollandica*

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C;Accession: S22469; S16850

R;Greer, K.L.; Golden, S.S.

Plant Mol. Biol. 19, 355-365, 1992

A;Title: Conserved relationship between psbH and petBD genes: presence of a
shared upstream element in *Prochlorothrix hollandica*.

A;Reference number: S22469; MUID:92322967; PMID:1623188

A;Accession: S22469

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <GRE>

A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVS 3
|||
Db 4 SVS 6

RESULT 40

C60683

malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - *tampala* (fragment)

N;Alternate names: NAD-malic enzyme

C;Species: *Amaranthus tricolor* (*tampala*)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-Feb-1997

C;Accession: C60683

R;Murata, T.; Ikeda, J.; Takano, M.; Ohsugi, R.

Plant Cell Physiol. 30, 429-437, 1989

A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.

A;Reference number: A60683

A;Accession: C60683

A;Molecule type: protein

A;Residues: 1-28 <MUR>

C;Keywords: NAD; oxidoreductase; photosynthesis

Query Match 8.8%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKG 12

|||

Db 25 NKG 27

Search completed: January 14, 2004, 10:37:23

Job time : 11.0623 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 22.8785 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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265	4	11.8	35	10	US-09-811-824-7	Sequence 7, Appli
266	4	11.8	35	11	US-09-983-802-486	Sequence 486, App
267	4	11.8	35	11	US-09-820-843A-106	Sequence 106, App
268	4	11.8	35	11	US-09-925-299-1258	Sequence 1258, Ap
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270	4	11.8	35	12	US-10-340-484-13	Sequence 13, Appl
271	4	11.8	35	12	US-10-062-599-138	Sequence 138, App
272	4	11.8	35	15	US-10-133-128-75	Sequence 75, Appl
273	4	11.8	35	15	US-10-062-831-138	Sequence 138, App
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282	4	11.8	36	14	US-10-002-344A-205	Sequence 205, App
283	4	11.8	36	15	US-10-050-704-192	Sequence 192, App
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290	4	11.8	37	12	US-10-340-783-16	Sequence 16, Appl
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292	4	11.8	37	12	US-10-339-740-265	Sequence 265, App
293	4	11.8	37	12	US-10-283-403-9	Sequence 9, Appli
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296	4	11.8	37	15	US-10-106-698-6085	Sequence 6085, Ap
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309	4	11.8	39	15	US-10-187-051-25	Sequence 25, Appl
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821	3	8.8	28	15	US-10-187-051-129	Sequence 129, App
822	3	8.8	28	15	US-10-187-051-131	Sequence 131, App
823	3	8.8	28	15	US-10-187-051-133	Sequence 133, App
824	3	8.8	28	15	US-10-187-051-135	Sequence 135, App
825	3	8.8	28	15	US-10-187-051-137	Sequence 137, App
826	3	8.8	28	15	US-10-187-051-139	Sequence 139, App
827	3	8.8	28	15	US-10-187-051-141	Sequence 141, App
828	3	8.8	28	15	US-10-187-051-143	Sequence 143, App
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834	3	8.8	28	15	US-10-187-051-163	Sequence 163, App
835	3	8.8	28	15	US-10-187-051-165	Sequence 165, App
836	3	8.8	28	15	US-10-023-282-626	Sequence 626, App
837	3	8.8	28	15	US-10-023-282-638	Sequence 638, App
838	3	8.8	28	15	US-10-023-282-1089	Sequence 1089, Ap
839	3	8.8	28	15	US-10-255-532-6	Sequence 6, Appli
840	3	8.8	28	15	US-10-075-869-24	Sequence 24, Appl
841	3	8.8	28	15	US-10-202-724-3	Sequence 3, Appli
842	3	8.8	28	15	US-10-262-017-3	Sequence 3, Appli
843	3	8.8	28	15	US-10-106-698-5608	Sequence 5608, Ap
844	3	8.8	28	15	US-10-106-698-6764	Sequence 6764, Ap
845	3	8.8	28	15	US-10-106-698-7736	Sequence 7736, Ap
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848	3	8.8	28	15	US-10-295-809-20	Sequence 20, Appl
849	3	8.8	28	15	US-10-322-579-2	Sequence 2, Appli
850	3	8.8	28	15	US-10-192-283A-12	Sequence 12, Appl
851	3	8.8	28	15	US-10-197-954-62	Sequence 62, Appl
852	3	8.8	28	15	US-10-197-954-145	Sequence 145, App
853	3	8.8	28	15	US-10-283-500-19	Sequence 19, Appl
854	3	8.8	28	15	US-10-295-981-23	Sequence 23, Appl

855	3	8.8	28	15	US-10-160-290-22	Sequence 22, Appl
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857	3	8.8	29	9	US-09-765-527-13	Sequence 13, Appl
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859	3	8.8	29	9	US-09-005-243-73	Sequence 73, Appl
860	3	8.8	29	9	US-09-904-380-23	Sequence 23, Appl
861	3	8.8	29	9	US-09-224-683-73	Sequence 73, Appl
862	3	8.8	29	9	US-09-932-161-1	Sequence 1, Appli
863	3	8.8	29	9	US-09-864-761-33834	Sequence 33834, A
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865	3	8.8	29	9	US-09-864-761-34337	Sequence 34337, A
866	3	8.8	29	9	US-09-864-761-35314	Sequence 35314, A
867	3	8.8	29	9	US-09-864-761-36235	Sequence 36235, A
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869	3	8.8	29	9	US-09-864-761-37579	Sequence 37579, A
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872	3	8.8	29	9	US-09-864-761-38222	Sequence 38222, A
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877	3	8.8	29	9	US-09-864-761-40727	Sequence 40727, A
878	3	8.8	29	9	US-09-864-761-40944	Sequence 40944, A
879	3	8.8	29	9	US-09-864-761-41199	Sequence 41199, A
880	3	8.8	29	9	US-09-864-761-41596	Sequence 41596, A
881	3	8.8	29	9	US-09-864-761-42035	Sequence 42035, A
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883	3	8.8	29	9	US-09-864-761-42342	Sequence 42342, A
884	3	8.8	29	9	US-09-864-761-42467	Sequence 42467, A
885	3	8.8	29	9	US-09-864-761-42832	Sequence 42832, A
886	3	8.8	29	9	US-09-864-761-42924	Sequence 42924, A
887	3	8.8	29	9	US-09-864-761-43064	Sequence 43064, A
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894	3	8.8	29	9	US-09-864-761-45777	Sequence 45777, A
895	3	8.8	29	9	US-09-864-761-45815	Sequence 45815, A
896	3	8.8	29	9	US-09-864-761-46618	Sequence 46618, A
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898	3	8.8	29	9	US-09-864-761-47383	Sequence 47383, A
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903	3	8.8	29	9	US-09-864-761-48746	Sequence 48746, A
904	3	8.8	29	9	US-09-876-388-22	Sequence 22, Appl
905	3	8.8	29	9	US-09-925-299-1270	Sequence 1270, Ap
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907	3	8.8	29	9	US-09-881-490-3	Sequence 3, Appli
908	3	8.8	29	9	US-09-789-836-13	Sequence 13, Appl
909	3	8.8	29	10	US-09-927-112-5	Sequence 5, Appli
910	3	8.8	29	10	US-09-927-112-6	Sequence 6, Appli
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913	3	8.8	29	10	US-09-872-864-19	Sequence 19, Appl
914	3	8.8	29	10	US-09-872-864-20	Sequence 20, Appl
915	3	8.8	29	10	US-09-922-261-258	Sequence 258, App
916	3	8.8	29	10	US-09-908-664-8	Sequence 8, Appli
917	3	8.8	29	10	US-09-908-664-9	Sequence 9, Appli
918	3	8.8	29	10	US-09-908-664-18	Sequence 18, Appl
919	3	8.8	29	10	US-09-905-831-12	Sequence 12, Appl
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921	3	8.8	29	10	US-09-003-869-79	Sequence 79, Appl
922	3	8.8	29	10	US-09-003-869-98	Sequence 98, Appl
923	3	8.8	29	10	US-09-911-969-7	Sequence 7, Appli
924	3	8.8	29	10	US-09-880-149-52	Sequence 52, Appl
925	3	8.8	29	10	US-09-880-149-55	Sequence 55, Appl
926	3	8.8	29	10	US-09-764-877-1395	Sequence 1395, Ap
927	3	8.8	29	10	US-09-071-838-189	Sequence 189, App
928	3	8.8	29	10	US-09-071-838-242	Sequence 242, App
929	3	8.8	29	10	US-09-956-206A-1	Sequence 1, Appli
930	3	8.8	29	10	US-09-984-245-227	Sequence 227, App
931	3	8.8	29	10	US-09-880-132-52	Sequence 52, Appl
932	3	8.8	29	10	US-09-880-132-55	Sequence 55, Appl
933	3	8.8	29	11	US-09-983-802-620	Sequence 620, App
934	3	8.8	29	11	US-09-956-940-38	Sequence 38, Appl
935	3	8.8	29	11	US-09-974-879-406	Sequence 406, App
936	3	8.8	29	11	US-09-974-879-511	Sequence 511, App
937	3	8.8	29	11	US-09-974-879-527	Sequence 527, App
938	3	8.8	29	11	US-09-259-658-15	Sequence 15, Appl
939	3	8.8	29	11	US-09-756-690A-79	Sequence 79, Appl
940	3	8.8	29	11	US-09-756-690A-98	Sequence 98, Appl
941	3	8.8	29	11	US-09-843-221A-152	Sequence 152, App
942	3	8.8	29	11	US-09-925-299-1270	Sequence 1270, Ap
943	3	8.8	29	11	US-09-847-102A-80	Sequence 80, Appl
944	3	8.8	29	11	US-09-813-153-218	Sequence 218, App
945	3	8.8	29	11	US-09-966-262-227	Sequence 227, App
946	3	8.8	29	11	US-09-969-730-196	Sequence 196, App
947	3	8.8	29	11	US-09-281-495-51	Sequence 51, Appl
948	3	8.8	29	11	US-09-983-966-227	Sequence 227, App
949	3	8.8	29	11	US-09-876-904A-28	Sequence 28, Appl
950	3	8.8	29	11	US-09-764-891-4191	Sequence 4191, Ap
951	3	8.8	29	11	US-09-764-891-4851	Sequence 4851, Ap
952	3	8.8	29	11	US-09-892-877-436	Sequence 436, App
953	3	8.8	29	11	US-09-847-208-125	Sequence 125, App
954	3	8.8	29	11	US-09-305-736-406	Sequence 406, App
955	3	8.8	29	11	US-09-305-736-512	Sequence 512, App
956	3	8.8	29	11	US-09-305-736-529	Sequence 529, App
957	3	8.8	29	11	US-09-095-478-25	Sequence 25, Appl
958	3	8.8	29	11	US-09-908-139-19	Sequence 19, Appl
959	3	8.8	29	11	US-09-908-139-21	Sequence 21, Appl
960	3	8.8	29	11	US-09-491-614-14	Sequence 14, Appl
961	3	8.8	29	11	US-09-491-614-15	Sequence 15, Appl
962	3	8.8	29	11	US-09-948-783-438	Sequence 438, App
963	3	8.8	29	11	US-09-910-082A-158	Sequence 158, App
964	3	8.8	29	11	US-09-910-082A-368	Sequence 368, App
965	3	8.8	29	12	US-10-153-604A-72	Sequence 72, Appl
966	3	8.8	29	12	US-10-231-894-44	Sequence 44, Appl
967	3	8.8	29	12	US-10-345-281-52	Sequence 52, Appl
968	3	8.8	29	12	US-10-345-281-55	Sequence 55, Appl

969	3	8.8	29	12	US-10-234-816-95	Sequence 95, Appl
970	3	8.8	29	12	US-09-789-831-13	Sequence 13, Appl
971	3	8.8	29	12	US-09-935-384-757	Sequence 757, App
972	3	8.8	29	12	US-09-935-384-758	Sequence 758, App
973	3	8.8	29	12	US-10-131-909A-7	Sequence 7, Appli
974	3	8.8	29	12	US-10-160-162-232	Sequence 232, App
975	3	8.8	29	12	US-10-096-777-1	Sequence 1, Appli
976	3	8.8	29	12	US-10-008-524A-123	Sequence 123, App
977	3	8.8	29	12	US-10-340-458-4	Sequence 4, Appli
978	3	8.8	29	12	US-10-340-458-21	Sequence 21, Appl
979	3	8.8	29	12	US-09-933-767-660	Sequence 660, App
980	3	8.8	29	12	US-09-933-767-1182	Sequence 1182, Ap
981	3	8.8	29	12	US-10-105-232-304	Sequence 304, App
982	3	8.8	29	12	US-10-105-232-319	Sequence 319, App
983	3	8.8	29	12	US-10-105-232-343	Sequence 343, App
984	3	8.8	29	12	US-10-105-232-512	Sequence 512, App
985	3	8.8	29	12	US-10-280-066-334	Sequence 334, App
986	3	8.8	29	12	US-10-289-135A-25	Sequence 25, Appl
987	3	8.8	29	12	US-10-029-386-27545	Sequence 27545, A
988	3	8.8	29	12	US-10-029-386-27995	Sequence 27995, A
989	3	8.8	29	12	US-10-029-386-29238	Sequence 29238, A
990	3	8.8	29	12	US-10-029-386-30063	Sequence 30063, A
991	3	8.8	29	12	US-10-029-386-31071	Sequence 31071, A
992	3	8.8	29	12	US-10-029-386-31232	Sequence 31232, A
993	3	8.8	29	12	US-10-029-386-31577	Sequence 31577, A
994	3	8.8	29	12	US-10-029-386-32473	Sequence 32473, A
995	3	8.8	29	12	US-10-029-386-32650	Sequence 32650, A
996	3	8.8	29	12	US-10-029-386-33620	Sequence 33620, A
997	3	8.8	29	12	US-10-189-437-291	Sequence 291, App
998	3	8.8	29	12	US-10-189-437-306	Sequence 306, App
999	3	8.8	29	12	US-10-189-437-330	Sequence 330, App
1000	3	8.8	29	12	US-10-189-437-499	Sequence 499, App

ALIGNMENTS

RESULT 1

US-09-843-221A-18

; Sequence 18, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

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; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18
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RESULT 2

Query Match 100.0%; Score 34; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

US-09-843-221A-41

; Sequence 41, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-41

Query Match 88.2%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

RESULT 4

US-09-843-221A-32

; Sequence 32, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 67.6%; Score 23; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.8e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
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Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 5

US-09-169-786-3

; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3

Query Match 67.6%; Score 23; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

US-09-928-047B-6

; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:

; APPLICANT: Cantor, Thomas
 ; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
 ; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
 ; FILE REFERENCE: 53221-20002.00
 ; CURRENT APPLICATION NUMBER: US/09/928,047B
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/224,446
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-047B-6

Query Match 67.6%; Score 23; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
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 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

US-09-843-221A-16

; Sequence 16, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-843-221A-16

Query Match 67.6%; Score 23; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-09-843-221A-17

; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

US-09-843-221A-20

; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A

```
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-20
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```
Query Match          67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          |||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34
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RESULT 10

US-09-843-221A-161

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; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
```

US-09-843-221A-161

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 11

US-09-843-221A-162

; Sequence 162, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 12

US-09-928-048A-6

; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1

; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

US-10-361-928-1

; Sequence 1, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-10-361-928-1

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

US-10-361-928-2

; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly

US-10-361-928-2

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-10-361-928-5

; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11

; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-5

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

US-10-361-928-8

; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-10-340-484-15

; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-10-340-484-16

; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-10-016-403-5

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: 1..34
;   OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

```

```

Query Match          67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches   23; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```

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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        |||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 20

US-10-016-403-6

```

; Sequence 6, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
;   APPLICANT: Holladay, Leslie A.
;   TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
;                       INCREASE ELECTROTRANSPORT FLUX
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
;       STREET: 25 West Main Street
;       CITY: Madison
;       STATE: WI
;       COUNTRY: USA
;       ZIP: 53701-2236
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/016,403
;       FILING DATE: 10-Dec-2001
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/466,610
;       FILING DATE: 1995-JUN-06
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Frenchick, Grady J.
;       REGISTRATION NUMBER: 29,018
;       REFERENCE/DOCKET NUMBER: 8734.28
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 608-257-2281
;       TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match 67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-10-097-079-1

; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808

```

; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 34 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: <Unknown>
;       TOPOLOGY: No. US20020132973A1 Relevant
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: N-terminal
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-079-1

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Query Match          67.6%;  Score 23;  DB 14;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.1e-16;
Matches   23;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

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RESULT 22
US-09-843-221A-15
; Sequence 15, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;   APPLICANT: KOSTENUIK, PAUL
;   APPLICANT: LIU, CHUAN-FA
;   APPLICANT: LACEY, DAVID LEE
;   TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
;   TITLE OF INVENTION: RELATED PROTEIN
;   FILE REFERENCE: A-665B
;   CURRENT APPLICATION NUMBER: US/09/843,221A
;   CURRENT FILING DATE: 2001-04-26
;   PRIOR APPLICATION NUMBER: 60/266,673
;   PRIOR FILING DATE: 2001-02-06
;   PRIOR APPLICATION NUMBER: 60/214,860
;   PRIOR FILING DATE: 2000-06-28
;   PRIOR APPLICATION NUMBER: 60/200,053
;   PRIOR FILING DATE: 2000-04-27
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-15

```

```

Query Match          67.6%;  Score 23;  DB 11;  Length 37;
Best Local Similarity 100.0%;  Pred. No. 1.2e-16;
Matches   23;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||||
Db      11 GKHLNSMERVEWLRKKLQDVHNF 33

```

RESULT 23

US-10-168-185-9

; Sequence 9, Application US/10168185
 ; Publication No. US20030175802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Armbruster, Franz Paul
 ; APPLICANT: Missbichler, Albert
 ; APPLICANT: Schmidt-Gayk, Heinrich
 ; APPLICANT: Roth, Heinz-Jurgen
 ; TITLE OF INVENTION: Method for Determining Parathormone
 ; TITLE OF INVENTION: Activity in a Human Sample
 ; FILE REFERENCE: HLZ-004US
 ; CURRENT APPLICATION NUMBER: US/10/168,185
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: PCT/EP00/12911
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: DE 19961350
 ; PRIOR FILING DATE: 1999-12-17
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-168-185-9

Query Match 67.6%; Score 23; DB 12; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

US-09-169-786-4

; Sequence 4, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-169-786-4

Query Match 67.6%; Score 23; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

US-09-843-221A-14

; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-14

Query Match 67.6%; Score 23; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 26

US-10-245-707-1

; Sequence 1, Application US/10245707
; Publication No. US20030171282A1
; GENERAL INFORMATION:
; APPLICANT: Patton, John S.
; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments of Parathyroid
Hormone
; FILE REFERENCE: 032055-047
; CURRENT APPLICATION NUMBER: US/10/245,707
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/577,264
; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 09/128,401
 ; PRIOR FILING DATE: 1998-08-03
 ; PRIOR APPLICATION NUMBER: US 08/625,586
 ; PRIOR FILING DATE: 1996-03-28
 ; PRIOR APPLICATION NUMBER: US 08/232,849
 ; PRIOR FILING DATE: 1994-04-25
 ; PRIOR APPLICATION NUMBER: US 07/953,397
 ; PRIOR FILING DATE: 1992-09-29
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: parathyroid hormone (PTH) fragment molecules
 US-10-245-707-1

Query Match 67.6%; Score 23; DB 12; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 27

US-10-361-928-3

; Sequence 3, Application US/10361928
 ; Publication No. US20030144209A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRINGHURST, F. RICHARD
 ; APPLICANT: TAKASU, HISASHI
 ; APPLICANT: GARDELLA, THOMAS J.
 ; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
 ; TITLE OF INVENTION: ANALOGS
 ; FILE REFERENCE: 0609.4630002
 ; CURRENT APPLICATION NUMBER: US/10/361,928
 ; CURRENT FILING DATE: 2003-02-11
 ; PRIOR APPLICATION NUMBER: 09/447,800
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: 60/110,152
 ; PRIOR FILING DATE: 1998-11-25
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: Desamino Gly
 US-10-361-928-3

Query Match 64.7%; Score 22; DB 12; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHN 33
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHN 33

RESULT 28

US-10-361-928-6

; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 64.7%; Score 22; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHN 33
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHN 33

RESULT 29

US-10-361-928-9

; Sequence 9, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002

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; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-9

```

```

Query Match          64.7%; Score 22; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHN 33
        ||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHN 33

```

RESULT 30

```

US-10-372-095-24
; Sequence 24, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-095-24

```

```

Query Match          61.8%; Score 21; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 GKHLNSMERVEWLRKKLQDVH 32
        ||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVH 32

```

RESULT 31

US-09-169-786-2

; Sequence 2, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-169-786-2

Query Match 58.8%; Score 20; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 32

US-09-843-221A-27

; Sequence 27, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 58.8%; Score 20; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33

```

; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-165

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Qy 12 GKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDV 31

; Sequence 39, Application US/09843221A
; Publication No. US20030039654A1

```
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39
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```
Query Match          55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      12 GKHLNSMERVEWLRKKLQD 30
          |||||
Db      12 GKHLNSMERVEWLRKKLQD 30
```

RESULT 35

```
US-09-843-221A-40
; Sequence 40, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 30
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-40

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 36

US-09-843-221A-43
; Sequence 43, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-43

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 37

US-09-843-221A-166
; Sequence 166, Application US/09843221A

; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
|||||
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 38

US-09-843-221A-34
; Sequence 34, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28

RESULT 40

US-09-843-221A-167

; Sequence 167, Application US/09843221A

: Publication No. US20030039654A1

; GENERAL INFORMATION:

: APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

7. TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

: TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

: PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

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; SOFTWARE: PatentIn version 3.1
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; SEO ID NO 167

; LENGTH: 29

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; TYPE: PRT
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: ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Preferred embodiments - PTH

```
; NAME/KEY: misc feature
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; LOCATION: (1) . (1)

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; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
```

US-09-843-221A-167

Query Match 52.9%; Score 18; DB 11; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.3e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQ 29

Db 12 GKHLNSMERVEWLRKKLQ 29

Search completed: January 14, 2004, 11:15:04

Job time : 23.8785 secs

1	9	26.5	31	11	Q91Y90	Q91y90 peromyscus
2	9	26.5	31	11	Q91Y91	Q91y91 peromyscus
3	5	14.7	34	5	O17148	O17148 echinococcu
4	5	14.7	34	16	Q97K50	Q97k50 clostridium
5	5	14.7	34	17	Q9HR65	Q9hr65 halobacteri
6	5	14.7	35	11	Q8BTB9	Q8btb9 mus musculu
7	5	14.7	35	16	Q97RG6	Q97rg6 streptococc
8	4	11.8	28	10	O24285	O24285 pinus radia
9	4	11.8	29	2	Q49148	Q49148 methylobact
10	4	11.8	29	4	Q9UCL2	Q9ucl2 homo sapien
11	4	11.8	29	5	Q25603	Q25603 onchocerca
12	4	11.8	29	8	Q9TI61	Q9ti61 allosyncarp
13	4	11.8	29	13	O13043	O13043 scyliorhinu
14	4	11.8	30	4	Q9UBV5	Q9ubv5 homo sapien
15	4	11.8	30	16	Q8DZP7	Q8dzp7 streptococc
16	4	11.8	31	1	Q55314	Q55314 sulfolobus
17	4	11.8	31	4	Q8NEI8	Q8nei8 homo sapien
18	4	11.8	31	16	O50669	O50669 borrelia bu
19	4	11.8	31	16	Q8EIW8	Q8eiw8 shewanella
20	4	11.8	32	11	Q9QZQ2	Q9qzq2 mus musculu
21	4	11.8	32	17	Q9HSZ0	Q9hsz0 halobacteri
22	4	11.8	33	5	Q95SD4	Q95sd4 drosophila
23	4	11.8	33	16	Q9PKX3	Q9pkx3 chlamydia m
24	4	11.8	34	2	Q9ZG81	Q9zg81 chlamydia t
25	4	11.8	34	2	Q8GFK2	Q8gfk2 staphylococ
26	4	11.8	34	11	Q8C4P4	Q8c4p4 mus musculu
27	4	11.8	34	13	Q90ZJ4	Q90zj4 gallus gall
28	4	11.8	34	16	Q98FK5	Q98fk5 rhizobium l
29	4	11.8	35	4	Q15421	Q15421 homo sapien
30	4	11.8	35	12	Q8V6J8	Q8v6j8 halovirus h
31	4	11.8	35	16	Q9KQG4	Q9kqg4 vibrio chol
32	4	11.8	35	16	Q8F102	Q8f102 leptospira
33	4	11.8	36	2	Q53920	Q53920 streptomyce
34	4	11.8	36	2	O68941	O68941 rhodospiril
35	4	11.8	36	4	Q8WXW8	Q8wxw8 homo sapien
36	4	11.8	36	10	Q9SJ63	Q9sj63 arabidopsis
37	4	11.8	36	12	Q9PXD1	Q9pxd1 hepatitis c
38	4	11.8	36	12	Q91D77	Q91d77 ttv-like mi
39	4	11.8	36	13	Q9YHT9	Q9yht9 brachydanio
40	4	11.8	36	16	Q97S91	Q97s91 streptococc
41	4	11.8	37	2	Q8KYJ0	Q8kyj0 bacillus an
42	4	11.8	37	5	Q9N2L2	Q9n2l2 caenorhabdi
43	4	11.8	37	10	Q39942	Q39942 helianthus
44	4	11.8	37	13	Q8AWW8	Q8aww8 oncorhynchu
45	4	11.8	37	16	Q8F6U2	Q8f6u2 leptospira
46	4	11.8	37	16	Q8F5H3	Q8f5h3 leptospira
47	4	11.8	37	16	Q8F419	Q8f419 leptospira
48	4	11.8	37	16	Q8EXV9	Q8exv9 leptospira
49	4	11.8	38	2	Q8KWH7	Q8kwh7 lactobacill
50	4	11.8	38	5	Q9NBE3	Q9nbe3 chironomus
51	4	11.8	38	5	Q9NBE5	Q9nbe5 chironomus
52	4	11.8	38	5	Q9NBE8	Q9nbe8 chironomus
53	4	11.8	38	5	Q9NBE4	Q9nbe4 chironomus
54	4	11.8	38	5	Q9NBE7	Q9nbe7 chironomus
55	4	11.8	38	11	O35918	O35918 rattus norv
56	4	11.8	38	11	Q91VC8	Q91vc8 mus musculu
57	4	11.8	38	13	Q8AWW9	Q8aww9 oncorhynchu

58	4	11.8	38	16	Q8E0D2	Q8e0d2 streptococc
59	4	11.8	39	2	Q8GPO8	Q8gpo8 pseudomonas
60	4	11.8	39	12	Q68847	Q68847 hepatitis c
61	4	11.8	39	12	Q68845	Q68845 hepatitis c
62	4	11.8	39	12	Q68846	Q68846 hepatitis c
63	4	11.8	39	13	Q90776	Q90776 gallus gall
64	4	11.8	39	16	Q9KYH4	Q9kyh4 streptomyce
65	4	11.8	39	16	Q8F0C7	Q8f0c7 leptospira
66	4	11.8	40	2	Q8GCS7	Q8gcs7 eubacterium
67	4	11.8	40	4	Q9UE56	Q9ue56 homo sapien
68	4	11.8	40	5	Q9NFH5	Q9nfh5 plasmodium
69	4	11.8	40	6	Q9N1X0	Q9nlx0 equus cabal
70	4	11.8	40	6	Q29283	Q29283 sus scrofa
71	4	11.8	40	12	Q91JZ7	Q91jz7 hepatitis c
72	3	8.8	28	2	Q01303	Q01303 treponema p
73	3	8.8	28	2	Q05574	Q05574 prochloroth
74	3	8.8	28	2	Q9ZB83	Q9zb83 vibrio angu
75	3	8.8	28	3	Q8TGN3	Q8tgn3 saccharomyc
76	3	8.8	28	3	Q8TGT8	Q8tgt8 saccharomyc
77	3	8.8	28	4	Q96SD9	Q96sd9 homo sapien
78	3	8.8	28	4	Q16326	Q16326 homo sapien
79	3	8.8	28	4	Q96EU0	Q96eu0 homo sapien
80	3	8.8	28	4	O75980	O75980 homo sapien
81	3	8.8	28	4	O95737	O95737 homo sapien
82	3	8.8	28	5	Q8MUW0	Q8muw0 schistosoma
83	3	8.8	28	5	Q8MPY2	Q8mpy2 caenorhabdi
84	3	8.8	28	5	Q9BJE4	Q9bje4 paupopus sp
85	3	8.8	28	6	O62821	O62821 bubalus bub
86	3	8.8	28	6	Q9XS89	Q9xs89 equus cabal
87	3	8.8	28	8	Q8WBC8	Q8wbc8 cucurbita e
88	3	8.8	28	8	Q9TIE9	Q9tie9 centella er
89	3	8.8	28	8	Q9TIE8	Q9tie8 centella as
90	3	8.8	28	8	Q9MR96	Q9mr96 crocodylus
91	3	8.8	28	8	Q9TIE6	Q9tie6 centella hi
92	3	8.8	28	8	Q9ZYS4	Q9zys4 leishmania
93	3	8.8	28	8	Q9MR94	Q9mr94 chelonia my
94	3	8.8	28	8	Q9TIE7	Q9tie7 centella tr
95	3	8.8	28	8	Q8HS23	Q8hs23 pisum sativ
96	3	8.8	28	8	Q8HS11	Q8hs11 spathiphyll
97	3	8.8	28	8	Q8HS07	Q8hs07 welwitschia
98	3	8.8	28	8	Q8HKF0	Q8hkf0 rhipicephal
99	3	8.8	28	9	Q9AZJ9	Q9azj9 bacterioph
100	3	8.8	28	9	Q38269	Q38269 bacterioph
101	3	8.8	28	10	Q8S526	Q8s526 ipomoea bat
102	3	8.8	28	10	Q8W232	Q8w232 zea mays (m
103	3	8.8	28	10	Q9LMD6	Q9lmd6 arabidopsis
104	3	8.8	28	11	Q9ESI4	Q9esi4 petromus ty
105	3	8.8	28	11	Q9ESI5	Q9esi5 thryonomys
106	3	8.8	28	11	Q9ESI6	Q9esi6 hystrix afr
107	3	8.8	28	11	Q99PL9	Q99pl9 mus musculu
108	3	8.8	28	11	Q9ESI2	Q9esi2 cryptomys h
109	3	8.8	28	11	Q9EP60	Q9ep60 heliophobi
110	3	8.8	28	11	Q9ESI0	Q9esi0 cryptomys s
111	3	8.8	28	11	Q91XP0	Q91xp0 rattus norv
112	3	8.8	28	11	P70651	P70651 mus sp. bet
113	3	8.8	28	11	Q9EP59	Q9ep59 georychus c
114	3	8.8	28	11	Q9ESI1	Q9esi1 cryptomys d

115	3	8.8	28	11	P97914	P97914 rattus norv
116	3	8.8	28	11	Q9EP61	Q9ep61 heteroceph
117	3	8.8	28	11	Q9ESH8	Q9esh8 bathyergus
118	3	8.8	28	11	Q9ESH9	Q9esh9 bathyergus
119	3	8.8	28	11	Q9QXB4	Q9qxb4 mus musculu
120	3	8.8	28	11	Q9ESI3	Q9esi3 cryptomys h
121	3	8.8	28	12	Q68087	Q68087 hepatitis c
122	3	8.8	28	12	Q67786	Q67786 human adeno
123	3	8.8	28	12	Q68095	Q68095 hepatitis c
124	3	8.8	28	12	Q68097	Q68097 hepatitis c
125	3	8.8	28	12	Q68092	Q68092 hepatitis c
126	3	8.8	28	12	Q68091	Q68091 hepatitis c
127	3	8.8	28	12	Q68093	Q68093 hepatitis c
128	3	8.8	28	12	Q68099	Q68099 hepatitis c
129	3	8.8	28	12	Q68096	Q68096 hepatitis c
130	3	8.8	28	12	Q68098	Q68098 hepatitis c
131	3	8.8	28	12	Q83181	Q83181 cauliflower
132	3	8.8	28	12	Q68086	Q68086 hepatitis c
133	3	8.8	28	12	Q68552	Q68552 hepatitis c
134	3	8.8	28	12	Q68094	Q68094 hepatitis c
135	3	8.8	28	12	Q9WNI4	Q9wni4 tt virus. o
136	3	8.8	28	13	Q9PRE8	Q9pre8 oryzias lat
137	3	8.8	28	13	Q9PRI9	Q9pri9 amia calva
138	3	8.8	28	13	Q9PRN8	Q9prn8 carassius a
139	3	8.8	28	15	O71346	O71346 human endog
140	3	8.8	28	15	Q9QEY3	Q9qey3 human immun
141	3	8.8	28	16	Q8X415	Q8x415 escherichia
142	3	8.8	28	16	Q8NVB8	Q8nvb8 staphylococ
143	3	8.8	28	16	Q8ENT7	Q8ent7 oceanobacil
144	3	8.8	28	16	Q8CK95	Q8ck95 yersinia pe
145	3	8.8	29	2	Q9ZGG4	Q9zgg4 heliobacill
146	3	8.8	29	2	Q54200	Q54200 streptomyce
147	3	8.8	29	2	Q9X3E3	Q9x3e3 prochloroco
148	3	8.8	29	2	Q9X3J9	Q9x3j9 prochloroco
149	3	8.8	29	2	Q47650	Q47650 escherichia
150	3	8.8	29	2	Q9AKV1	Q9akv1 neisseria g
151	3	8.8	29	2	Q9R511	Q9r511 bacillus su
152	3	8.8	29	2	Q8GL27	Q8gl27 borrelia bu
153	3	8.8	29	3	P78747	P78747 saccharomyc
154	3	8.8	29	3	Q8TGQ5	Q8tgq5 saccharomyc
155	3	8.8	29	4	Q9Y3G1	Q9y3g1 homo sapien
156	3	8.8	29	4	Q9H2A1	Q9h2a1 homo sapien
157	3	8.8	29	4	Q9UN87	Q9un87 homo sapien
158	3	8.8	29	4	Q9UDJ9	Q9udj9 homo sapien
159	3	8.8	29	4	Q9H465	Q9h465 homo sapien
160	3	8.8	29	4	Q8NEF6	Q8nef6 homo sapien
161	3	8.8	29	4	Q8TDW8	Q8tdw8 homo sapien
162	3	8.8	29	4	Q96IR5	Q96ir5 homo sapien
163	3	8.8	29	4	Q9BSQ3	Q9bsq3 homo sapien
164	3	8.8	29	5	Q95VB2	Q95vb2 spirometra
165	3	8.8	29	5	Q95NF4	Q95nf4 drosophila
166	3	8.8	29	5	Q24683	Q24683 dugesia tig
167	3	8.8	29	6	Q95MD3	Q95md3 bos taurus
168	3	8.8	29	6	Q9TRG5	Q9trg5 sus scrofa
169	3	8.8	29	8	Q8WBB9	Q8wbb9 cucurbita f
170	3	8.8	29	8	Q9TI57	Q9ti57 corymbia pa
171	3	8.8	29	8	Q8W7W7	Q8w7w7 cucurbita p

172	3	8.8	29	8	Q9GF70	Q9gf70 trochodendr
173	3	8.8	29	8	Q8W7W4	Q8w7w4 cucurbita a
174	3	8.8	29	8	Q8W7W6	Q8w7w6 cucurbita p
175	3	8.8	29	8	Q8WBC1	Q8wbc1 cucurbita o
176	3	8.8	29	8	Q9B5Z6	Q9b5z6 pseudostylo
177	3	8.8	29	8	Q8W7W5	Q8w7w5 cucurbita p
178	3	8.8	29	8	Q9B938	Q9b938 eupristina
179	3	8.8	29	8	Q9G370	Q9g370 draco blanf
180	3	8.8	29	8	Q8WBD0	Q8wbd0 cucurbita a
181	3	8.8	29	8	Q8WBB6	Q8wbb6 citrullus l
182	3	8.8	29	8	Q8W7W9	Q8w7w9 cucurbita f
183	3	8.8	29	8	Q8W7W8	Q8w7w8 cucurbita m
184	3	8.8	29	8	Q8HS21	Q8hs21 rheum x cul
185	3	8.8	29	9	Q9FZX6	Q9fzx6 bacterioph
186	3	8.8	29	10	Q9SC62	Q9sc62 picea abies
187	3	8.8	29	10	Q9SC58	Q9sc58 picea abies
188	3	8.8	29	10	Q9FUS3	Q9fus3 physcomitre
189	3	8.8	29	10	Q9SC57	Q9sc57 picea abies
190	3	8.8	29	10	P82196	P82196 spinacia ol
191	3	8.8	29	11	Q9JK05	Q9jk05 mus musculu
192	3	8.8	29	11	Q9Z2C0	Q9z2c0 mus musculu
193	3	8.8	29	11	Q921Z6	Q921z6 mus musculu
194	3	8.8	29	11	Q9Z2C1	Q9z2c1 mus musculu
195	3	8.8	29	11	O70564	O70564 mus musculu
196	3	8.8	29	11	Q9QY65	Q9qy65 mus musculu
197	3	8.8	29	11	Q62300	Q62300 mus musculu
198	3	8.8	29	11	O08980	O08980 mus musculu
199	3	8.8	29	11	Q8CGM8	Q8cgm8 mus musculu
200	3	8.8	29	12	Q91HB1	Q91hb1 porcine cir
201	3	8.8	29	12	O92646	O92646 hepatitis e
202	3	8.8	29	12	Q919A5	Q919a5 porcine rep
203	3	8.8	29	12	Q919A7	Q919a7 porcine rep
204	3	8.8	29	12	Q86872	Q86872 cauliflower
205	3	8.8	29	12	O92648	O92648 hepatitis e
206	3	8.8	29	12	O56835	O56835 vibrio chol
207	3	8.8	29	13	Q8AYR0	Q8ayr0 oryzias lat
208	3	8.8	29	13	Q8AWC2	Q8awc2 gallus gall
209	3	8.8	29	15	O72001	O72001 human endog
210	3	8.8	29	15	O71342	O71342 human endog
211	3	8.8	29	15	O71339	O71339 human endog
212	3	8.8	29	15	O71347	O71347 human endog
213	3	8.8	29	15	O71340	O71340 human endog
214	3	8.8	29	15	O71343	O71343 human endog
215	3	8.8	29	15	Q9IQJ8	Q9iqj8 human immun
216	3	8.8	29	15	O71991	O71991 human endog
217	3	8.8	29	15	Q9IQJ1	Q9iqj1 human immun
218	3	8.8	29	15	O71994	O71994 human endog
219	3	8.8	29	15	O71341	O71341 human endog
220	3	8.8	29	15	O71345	O71345 human endog
221	3	8.8	29	15	O71336	O71336 human endog
222	3	8.8	29	15	O71344	O71344 human endog
223	3	8.8	29	15	O71338	O71338 human endog
224	3	8.8	29	15	O71992	O71992 human endog
225	3	8.8	29	15	O71337	O71337 human endog
226	3	8.8	29	15	Q9IQJ9	Q9iqj9 human immun
227	3	8.8	29	15	O71997	O71997 human endog
228	3	8.8	29	15	O71335	O71335 human endog

Q8x419	escherichia	229	3	8.8	29	16	Q8X419
Q8q0h5	methanosarc	230	3	8.8	29	17	Q8Q0H5
Q9jp75	salmoneila	231	3	8.8	30	2	Q9JP75
Q9l8w9	streptomyce	232	3	8.8	30	2	Q9L8W9
Q9l8x1	streptomyce	233	3	8.8	30	2	Q9L8X1
Q9r4z6	clostridium	234	3	8.8	30	2	Q9R4Z6
Q9rei5	acidiphilii	235	3	8.8	30	2	Q9REI5
Q9r4j2	helicobacte	236	3	8.8	30	2	Q9R4J2
Q8vuw9	staphylococ	237	3	8.8	30	2	Q8VUW9
Q9r4i5	mycoplasma	238	3	8.8	30	2	Q9R4I5
Q9r4a9	clostridium	239	3	8.8	30	2	Q9R4A9
Q9r5q3	leuconostoc	240	3	8.8	30	2	Q9R5Q3
Q45966	coxiella bu	241	3	8.8	30	2	Q45966
Q9r5c4	comamonas	242	3	8.8	30	2	Q9R5C4
Q9s0i4	borrelia bu	243	3	8.8	30	2	Q9S0I4
Q9r4i6	mycoplasma	244	3	8.8	30	2	Q9R4I6
Q9r4a8	clostridium	245	3	8.8	30	2	Q9R4A8
Q9rer6	enterobacte	246	3	8.8	30	2	Q9REr6
Q9p8i7	candida alb	247	3	8.8	30	3	Q9P8I7
Q9urb0	candida alb	248	3	8.8	30	3	Q9URB0
Q8j172	trichoderma	249	3	8.8	30	3	Q8J172
Q8j171	hypocrea li	250	3	8.8	30	3	Q8J171
Q16330	homo sapien	251	3	8.8	30	4	Q16330
Q9uca9	homo sapien	252	3	8.8	30	4	Q9UCA9
Q95595	homo sapien	253	3	8.8	30	4	Q95595
P78460	homo sapien	254	3	8.8	30	4	P78460
Q8n563	homo sapien	255	3	8.8	30	4	Q8N563
Q9hbg2	homo sapien	256	3	8.8	30	4	Q9HBG2
Q9bzn2	homo sapien	257	3	8.8	30	4	Q9BZN2
P78542	homo sapien	258	3	8.8	30	4	P78542
Q9twh7	ancylostoma	259	3	8.8	30	5	Q9TWH7
Q968n1	tritric homo	260	3	8.8	30	5	Q968N1
P82214	bombyx mori	261	3	8.8	30	5	P82214
Q9bdk1	bos taurus	262	3	8.8	30	6	Q9BDK1
Q9tTF9		263	3	8.8	30	6	Q9TTF9
Q8w7L1		264	3	8.8	30	8	Q8W7L1
Q8w7K9		265	3	8.8	30	8	Q8W7K9
Q8w7H8		266	3	8.8	30	8	Q8W7H8
Q8wBC2		267	3	8.8	30	8	Q8WBC2
Q8w7K8		268	3	8.8	30	8	Q8W7K8
Q8w7H6		269	3	8.8	30	8	Q8W7H6
Q8wBC4		270	3	8.8	30	8	Q8WBC4
Q8w7L2		271	3	8.8	30	8	Q8W7L2
Q8wBC6		272	3	8.8	30	8	Q8WBC6
Q8wbb7	sechium edu	273	3	8.8	30	8	Q8WBB7
Q99328	meloidogyne	274	3	8.8	30	8	Q99328
Q8w7h7	cucurbita e	275	3	8.8	30	8	Q8W7H7
Q8wBC0	cucurbita f	276	3	8.8	30	8	Q8WBC0
Q8w7L0	cucurbita p	277	3	8.8	30	8	Q8W7L0
Q9ti56	eucalyptus	278	3	8.8	30	8	Q9TI56
Q8hkg1	rhipidcephal	279	3	8.8	30	8	Q8HKG1
Q8w674	enterobacte	280	3	8.8	30	9	Q8W674
Q9s8t2	cicer ariet	281	3	8.8	30	10	Q9S8T2
023933	flaveria tr	282	3	8.8	30	10	023933
Q9fusi	physcomitre	283	3	8.8	30	10	Q9FUS1
Q8rudi	zea mays (m	284	3	8.8	30	10	Q8RUD1
Q93wy2	oryza sativ	285	3	8.8	30	10	Q93WY2

Q63885	mus sp. cys	088549	mesocricetu	Q8vd11	mus musculu	Q9qv18	ratus sp.	Q9qv14	mus sp. col	Q9qv19	ratus sp.	Q10753	ratus norv	Q8br32	mus musculu	Q91hb7	tt virus. o	Q91hc4	tt virus. o	Q91jv5	norwalk vir	Q86870	cauliflower	Q91hc3	tt virus. o	Q91k3	hepatitis e	Q91hc0	tt virus. o	042551	brachydantio	Q98ue7	xenopus lae	Q9prw0	struthio ca	Q9pt00	oncorhynchu	Q86599	human endog	Q991p5	human immun	050822	borrelia bu	Q9x0w9	thermotoga	Q9p53	campylobact	Q9ku55	vibrio chol	Q9kt75	vibrio chol	Q9ksa7	vibrio chol	Q9jsq6	neisseria m	Q97sy9	streptococc	Q97sx5	streptococc	Q9k1w7	chlamydia p	Q8u566	agrobacteri	Q8kes5	chlorobium	Q8g1r1	brucella su	Q8ftzx9	brucella su	Q8cu88	staphylococ	Q8zzf0	pyrobaculum	Q8zv10	pyrobaculum	Q9s619	prochloroco	Q8kyk0	bacillus an	Q9jmw2	escherichia	Q9x3c3	prochloroco	068825	pseudomonas	Q9kh08	thermus aqu	Q47323	escherichia	Q9thf9	actinobact	Q8ky19	bacillus an	Q8rts5	uncultured	Q8l3d3	colwellia m	Q93pel	yersinia ps	094120	saccharomyc	Q96a45	homo sapien	Q9uea9	homo sapien	Q8wyf5	homo sapien	Q8n5x3	homo sapien	Q9bxxm4	homo sapien	Q9udes	homo sapien																																													
286	3	8.8	30	11	Q63885	30	11	Q90V14	30	11	Q90V19	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
287	3	8.8	30	11	088549	30	11	Q8VDL1	30	11	Q9QV18	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
288	3	8.8	30	11	Q8VDL1	30	11	Q9QV18	30	11	Q9QV19	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
289	3	8.8	30	11	Q9QV18	30	11	Q9QV14	30	11	Q9QV19	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
290	3	8.8	30	11	Q9QV18	30	11	Q9QV14	30	11	Q9QV19	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
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292	3	8.8	30	11	Q9QV18	30	11	Q9QV14	30	11	Q9QV19	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
293	3	8.8	30	11	Q9QV18	30	11	Q9QV14	30	11	Q9QV19	30	11	Q10753	30	11	Q8BR32	30	12	Q91HB7	30	12	Q91HC4	30	12	Q91Jv5	30	12	Q86870	30	12	Q91HC0	30	13	Q42551	30	13	Q98UE7	30	13	Q9PRW0	30	13	Q9PT00	30	15	Q86599	30	15	Q991P5	30	16	050822	30	16	Q9XW09	30	16	Q9PP53	30	16	Q9KU55	30	16	Q9KT75	30	16	Q9KSA7	30	16	Q9JSQ6	30	16	Q97SY9	30	16	Q97SX5	30	16	Q9K1W7	30	16	Q8U566	30	16	Q8KE55	30	16	Q8G1R1	30	16	Q8FZX9	30	16	Q8CU88	30	17	Q8ZZF0	30	17	Q8ZVL0	31	2	Q9S619	31	2	Q8KYK0	31	2	Q9JMV2	31	2	Q9X3C3	31	2	068825	31	2	Q9KH08	31	2	Q47323	31	2	Q9RHP9	31	2	Q8KYI9	31	2	Q8RTS5	31	2	Q8L3D3	31	2	Q93PE1	31	3	094120	31	4	Q96A45	31	4	Q9UEA9	31	4	Q8WYF5	31	4	Q8N5X3	31	4	Q9BXM4	31	4	Q9UDES
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Q81qV3	drosophila	343	3	8.8	31	5	Q8IQV3
Q81ey3	trypanosoma	344	3	8.8	31	5	Q8IEY3
Q9GLD6	sus scrofa	345	3	8.8	31	6	Q9GLD6
Q8mih5	canis faml	346	3	8.8	31	6	Q8MIH5
Q776Z5	bos taurus	347	3	8.8	31	6	Q776Z5
Q951C0	sus scrofa	348	3	8.8	31	6	Q951C0
Q9N1C8	ovis aries	349	3	8.8	31	6	Q9N1C8
Q9XSB9	ateles belz	350	3	8.8	31	6	Q9XSB9
Q97800	bos taurus	351	3	8.8	31	6	Q97800
Q29868	homo sapien	352	3	8.8	31	7	Q29868
Q9MNM2	buto americ	353	3	8.8	31	8	Q9MNM2
Q80011	enallagma a	354	3	8.8	31	8	Q80011
Q349Z2	limulus pol	355	3	8.8	31	8	Q349Z2
Q8WEJ4	gnetum gnet	356	3	8.8	31	8	Q8WEJ4
Q8m9Y3	chaetosphae	357	3	8.8	31	8	Q8M9Y3
Q9mnl2	torrentophr	358	3	8.8	31	8	Q9MNL2
Q9ms78	phacus acum	359	3	8.8	31	8	Q9MS78
Q9mnl3	torrentophr	360	3	8.8	31	8	Q9MNL3
Q38499	bacterioph	361	3	8.8	31	9	Q38499
Q9XIT0	glycine max	362	3	8.8	31	10	Q9XIT0
Q9QXB6	mus musculu	363	3	8.8	31	11	Q9QXB6
Q99KK6	mus musculu	364	3	8.8	31	11	Q99KK6
Q922Z6	mus musculu	365	3	8.8	31	11	Q922Z6
Q8CGM7	mus musculu	366	3	8.8	31	11	Q8CGM7
Q919E5	human papil	367	3	8.8	31	12	Q919E5
Q919E4	human papil	368	3	8.8	31	12	Q919E4
Q56713	hepatitis c	369	3	8.8	31	12	Q56713
Q919F7	human papil	370	3	8.8	31	12	Q919F7
Q919E6	human papil	371	3	8.8	31	12	Q919E6
Q56692	hepatitis c	372	3	8.8	31	12	Q56692
Q919F3	human papil	373	3	8.8	31	12	Q919F3
Q56707	hepatitis c	374	3	8.8	31	12	Q56707
Q56687	hepatitis c	375	3	8.8	31	12	Q56687
Q919F8	human papil	376	3	8.8	31	12	Q919F8
Q56691	hepatitis c	377	3	8.8	31	12	Q56691
Q919E1	human papil	378	3	8.8	31	12	Q919E1
Q56701	hepatitis c	379	3	8.8	31	12	Q56701
Q56694	hepatitis c	380	3	8.8	31	12	Q56694
Q919D9	human papil	381	3	8.8	31	12	Q919D9
Q919F6	human papil	382	3	8.8	31	12	Q919F6
Q919E3	human papil	383	3	8.8	31	12	Q919E3
Q56712	hepatitis c	384	3	8.8	31	12	Q56712
Q919E8	human papil	385	3	8.8	31	12	Q919E8
Q56710	hepatitis c	386	3	8.8	31	12	Q56710
Q56688	hepatitis c	387	3	8.8	31	12	Q56688
Q56696	hepatitis c	388	3	8.8	31	12	Q56696
Q56695	hepatitis c	389	3	8.8	31	12	Q56695
Q56698	hepatitis c	390	3	8.8	31	12	Q56698
Q56702	hepatitis c	391	3	8.8	31	12	Q56702
Q56703	hepatitis c	392	3	8.8	31	12	Q56703
Q56697	hepatitis c	393	3	8.8	31	12	Q56697
Q919F0	human papil	394	3	8.8	31	12	Q919F0
Q56709	hepatitis c	395	3	8.8	31	12	Q56709
Q919F4	human papil	396	3	8.8	31	12	Q919F4
Q56689	hepatitis c	397	3	8.8	31	12	Q56689
Q919F2	human papil	398	3	8.8	31	12	Q919F2
Q919F1	human papil	399	3	8.8	31	12	Q919F1

400	3	8.8	31	12	056711
401	3	8.8	31	12	Q919E2
402	3	8.8	31	12	Q919D8
403	3	8.8	31	12	056686
404	3	8.8	31	12	Q9WMX5
405	3	8.8	31	12	056690
406	3	8.8	31	12	Q919E9
407	3	8.8	31	12	056706
408	3	8.8	31	12	056700
409	3	8.8	31	12	056704
410	3	8.8	31	12	Q919D7
411	3	8.8	31	12	Q919F5
412	3	8.8	31	12	056693
413	3	8.8	31	12	056685
414	3	8.8	31	12	056708
415	3	8.8	31	12	Q919E0
416	3	8.8	31	12	056705
417	3	8.8	31	12	Q919E7
418	3	8.8	31	12	Q914M9
419	3	8.8	31	12	056699
420	3	8.8	31	13	042540
421	3	8.8	31	13	Q91763
422	3	8.8	31	13	Q9P5U1
423	3	8.8	31	13	Q91816
424	3	8.8	31	16	050709
425	3	8.8	31	16	050818
426	3	8.8	31	16	050858
427	3	8.8	31	16	051007
428	3	8.8	31	16	Q9PGF2
429	3	8.8	31	16	Q9PAW4
430	3	8.8	31	16	Q9KVF3
431	3	8.8	31	16	Q9KR17
432	3	8.8	31	16	Q9K7A8
433	3	8.8	31	16	Q97SZ9
434	3	8.8	31	16	Q97SW8
435	3	8.8	31	16	Q97QB7
436	3	8.8	31	16	Q97CV6
437	3	8.8	31	16	Q9K2A0
438	3	8.8	31	16	Q9K236
439	3	8.8	31	16	Q8U5M9
440	3	8.8	31	16	Q8P9W1
441	3	8.8	31	16	Q8KEV8
442	3	8.8	31	16	Q8KCQ0
443	3	8.8	31	16	Q8KCD4
444	3	8.8	31	16	Q8KBJ8
445	3	8.8	31	16	Q8EI77
446	3	8.8	31	16	Q8EG38
447	3	8.8	31	16	Q8E9Y5
448	3	8.8	31	16	Q8E8G1
449	3	8.8	31	16	Q8CTW3
450	3	8.8	31	16	Q8CTA2
451	3	8.8	32	2	Q9AJ41
452	3	8.8	32	2	Q00491
453	3	8.8	32	2	Q49249
454	3	8.8	32	2	Q44499
455	3	8.8	32	2	Q9S629
456	3	8.8	32	2	Q8KYN3
056711	hepatitis c				
Q919e2	human papil				
Q919d8	human papil				
056686	hepatitis c				
Q9wmx5	human echov				
056690	hepatitis c				
Q919e9	human papil				
056706	hepatitis c				
056700	hepatitis c				
056704	hepatitis c				
Q919d7	human papil				
Q919f5	human papil				
056693	hepatitis c				
056685	hepatitis c				
056708	hepatitis c				
Q919e0	human papil				
056705	hepatitis c				
Q919e7	human papil				
Q914m9	sulfolobus				
056699	hepatitis c				
042540	brachydanio				
Q91763	xenopus lae				
Q9p5u1	xenopus lae				
Q91816	xenopus lae				
050709	borrelia bu				
050818	borrelia bu				
050858	borrelia bu				
051007	borrelia bu				
Q9pgf2	xylella fas				
Q9paw4	xylella fas				
Q9kvt3	vibrio chol				
Q9kr17	vibrio chol				
Q9k7a8	bacillus ha				
Q97sz9	streptococc				
Q97sw8	streptococc				
Q97qb7	streptococc				
Q97cv6	streptococc				
Q9k2a0	chlamydia p				
Q9k236	chlamydia p				
Q8u5m9	agrobacteri				
Q8p9w1	xanthomonas				
Q8kev8	chlorobium				
Q8kcq0	chlorobium				
Q8kcd4	chlorobium				
Q8kbj8	chlorobium				
Q8ei77	shewanella				
Q8eg38	shewanella				
Q8e9y5	shewanella				
Q8e8g1	shewanella				
Q8ctw3	staphylococ				
Q8cta2	staphylococ				
Q9aj41	buchnera ap				
Q00491	streptomyce				
Q49249	mycoplasma				
Q44499	anabaena va				
Q9s629	prochloroco				
Q8kyn3	bacillus an				

044509	azotobacter	044509	32	2	8.8	3	457
045534	bacillus su	045534	32	2	8.8	3	458
08vn21	kluyvera ci	08VN21	32	2	8.8	3	459
09r5q7	aeromonas h	09R5Q7	32	2	8.8	3	460
08kym4	bacillus an	08KYM4	32	2	8.8	3	461
032493	bacteroides	032493	32	2	8.8	3	462
08vnt6	enterobacte	08VNT6	32	2	8.8	3	463
091373	rhizobium l	091373	32	2	8.8	3	464
08gf58	zymomonas m	08GFF58	32	2	8.8	3	465
001058	kluyveromyc	001058	32	3	8.8	3	466
08tgr3	saccharomyc	08TGT3	32	3	8.8	3	467
012900	homo sapien	012900	32	4	8.8	3	468
09ueb0	homo sapien	09UEB0	32	4	8.8	3	469
08tc25	homo sapien	08TC25	32	4	8.8	3	470
096gm7	homo sapien	096GM7	32	4	8.8	3	471
08tbq3	homo sapien	08TBQ3	32	4	8.8	3	472
096i20	homo sapien	096I20	32	4	8.8	3	473
09un69	homo sapien	09UN69	32	4	8.8	3	474
09uqvl	homo sapien	09UQVL	32	4	8.8	3	475
09gpd9	drosoophila	09GPD9	32	5	8.8	3	476
08tc382	leishmania	08TC382	32	5	8.8	3	477
096634	trypanosoma	096634	32	5	8.8	3	478
09rtwr8	procambarus	09RTWR8	32	5	8.8	3	479
018606	branchiosto	018606	32	5	8.8	3	480
08t757	branchiosto	08T757	32	5	8.8	3	481
09tr67	sus scrofa	09TR67	32	6	8.8	3	482
09tr69	sus scrofa	09TR69	32	6	8.8	3	483
09tse6	oryctolagus	09TSE6	32	6	8.8	3	484
08mj91	macaca mula	08MJ91	32	6	8.8	3	485
08snf1	gallinago m	08SNF1	32	7	8.8	3	486
019722	homo sapien	019722	32	7	8.8	3	487
036494	farfantepen	036494	32	8	8.8	3	488
08sl89	euglena ste	08SL89	32	8	8.8	3	489
09gcf95	cercidiphyll	09GCF95	32	8	8.8	3	490
031736	beta vulgar	031736	32	8	8.8	3	491
08sl87	euglena vir	08SL87	32	8	8.8	3	492
031735	beta vulgar	031735	32	8	8.8	3	493
09mm0	bufo andrew	09MM0	32	8	8.8	3	494
09mnl0	bufo danate	09MNL0	32	8	8.8	3	495
0951q4	renilla ren	0951Q4	32	8	8.8	3	496
09gft72	saururus ce	09GFT72	32	8	8.8	3	497
09mbu5	chlamydia p	09MBU5	32	9	8.8	3	498
08s527	ipomoea bat	08S527	32	10	8.8	3	499
08rxq5	arabidopsis	08RXQ5	32	10	8.8	3	500
040727	oryza sativ	040727	32	10	8.8	3	501
09j1ui	rattus norv	09J1UI	32	11	8.8	3	502
09roez	mus musculu	09ROM2	32	11	8.8	3	503
09qwm2	mus musculu	09QWM2	32	11	8.8	3	504
09qwb2	rattus sp.	09QWB2	32	11	8.8	3	505
09qxx1	mus musculu	09QXX1	32	11	8.8	3	506
08c2n8	mus musculu	08C2N8	32	11	8.8	3	507
09pav2	hepatitis b	09PAXV2	32	12	8.8	3	508
09wnis	tt virus. o	09WNIS	32	12	8.8	3	509
0914f9	sulfolobus	0914F9	32	12	8.8	3	510
08qytc4	grapevine v	08QYTC4	32	12	8.8	3	511
08qytc7	grapevine v	08QYTC7	32	12	8.8	3	512
066854	foot-and-mo	066854	32	12	8.8	3	513

Q8qyu0	grapevine v	Q8qyU0	32	12	3	8.8
Q9q934	shope fibro	Q9Q934	32	12	3	8.8
Q8qg73	oncorhynchu	Q8Qg73	32	13	3	8.8
Q8qg72	salmo salar	Q8Qg72	32	13	3	8.8
Q8qg71	oncorhynchu	Q8Qg71	32	13	3	8.8
Q9ps21	carassius a	Q9PS21	32	13	3	8.8
Q8qg84	oncorhynchu	Q8Qg84	32	13	3	8.8
Q8qg83	oncorhynchu	Q8Qg83	32	13	3	8.8
Q8qg82	oncorhynchu	Q8Qg82	32	13	3	8.8
Q8qg70	salvelinus	Q8Qg70	32	13	3	8.8
050706	borrelia bu	050706	32	16	3	8.8
050851	borrelia bu	050851	32	16	3	8.8
050865	borrelia bu	050865	32	16	3	8.8
051003	borrelia bu	051003	32	16	3	8.8
Q9pgt0	xylella fas	Q9PGT0	32	16	3	8.8
Q9kvt7	vibriu chol	Q9KVF7	32	16	3	8.8
Q9kvt2	vibriu chol	Q9KTV2	32	16	3	8.8
Q9kpn9	vibriu chol	Q9KPN9	32	16	3	8.8
Q9klt0	vibriu chol	Q9KLT0	32	16	3	8.8
Q9k7b0	bacillus ha	Q9K7B0	32	16	3	8.8
Q9a2h0	caulobacter	Q9A2H0	32	16	3	8.8
Q98ab6	rhizobium l	Q98AB6	32	16	3	8.8
Q8x3v6	escherichia	Q8X3V6	32	16	3	8.8
Q8p382	xanthomonas	Q8P382	32	16	3	8.8
Q8kg49	chlorobium	Q8KG49	32	16	3	8.8
Q8kez9	chlorobium	Q8KEZ9	32	16	3	8.8
Q8kcv3	chlorobium	Q8KCV3	32	16	3	8.8
Q9k4g0	streptomyce	Q9K4G0	32	16	3	8.8
Q8ej44	shewanella	Q8EJ44	32	16	3	8.8
Q8ee22	shewanella	Q8EE22	32	16	3	8.8
Q8ead5	shewanella	Q8EAD5	32	16	3	8.8
Q8cu60	staphylococ	Q8CU60	32	16	3	8.8
Q8ctr7	staphylococ	Q8CTR7	32	16	3	8.8
Q8cre7	staphylococ	Q8CRE7	32	16	3	8.8
Q8zzf7	pyrobaculum	Q8ZZF7	32	17	3	8.8
Q8kh96	pseudomonas	Q8KH96	33	2	3	8.8
Q9s624	prochloporo	Q9S624	33	2	3	8.8
Q9r2m3	prochloporo	Q9R2M3	33	2	3	8.8
Q9x3m5	prochloporo	Q9X3M5	33	2	3	8.8
Q9s651	streptococc	Q9S651	33	2	3	8.8
Q9k533	listeria mo	Q9K533	33	2	3	8.8
Q9k370	rhizobium l	Q9K370	33	2	3	8.8
Q9f2c4	salmonella	Q9F2C4	33	2	3	8.8
Q8kg80	vibriu chol	Q8KQ80	33	2	3	8.8
Q56414	escherichia	Q56414	33	2	3	8.8
Q9s622	prochloporo	Q9S622	33	2	3	8.8
Q9k2v1	rhizobium l	Q9K2V1	33	2	3	8.8
Q9f1f4	enterococcu	Q9F1F4	33	2	3	8.8
P82583	streptococc	P82583	33	2	3	8.8
Q8gl15	borrelia bu	Q8GL15	33	2	3	8.8
Q8tgr1	saccharomyc	Q8TGR1	33	3	3	8.8
Q99950	homo sapien	Q99950	33	4	3	8.8
Q9uc33	homo sapien	Q9UC33	33	4	3	8.8
Q9up36	homo sapien	Q9UP36	33	4	3	8.8
Q15285	homo sapien	Q15285	33	4	3	8.8
Q9udi1	homo sapien	Q9UDI1	33	4	3	8.8
Q8n4j9	homo sapien	Q8N4J9	33	4	3	8.8

Q92668	homo sapien	092668	33	4	8.8
Q92672	eimeria ten	Q9G7B2	33	5	8.8
Q92673	cryptospori	Q9GT93	33	5	8.8
Q26673	tethya aura	Q26673	33	5	8.8
Q26672	tethya aura	Q26672	33	5	8.8
Q9gtc2	plasmodium	Q9GTC2	33	5	8.8
Q9gtb3	eimeria ten	Q9G7B3	33	5	8.8
Q9gta6	sarcocystis	Q9GTA6	33	5	8.8
Q9gtal	babesia bov	Q9GTA1	33	5	8.8
Q17293	cancer ante	Q17293	33	5	8.8
Q27310	paramecium	Q27310	33	5	8.8
Q9gta9	sarcocystis	Q9GTA9	33	5	8.8
Q9gt95	cryptospori	Q9GT95	33	5	8.8
Q9gta2	babesia bov	Q9GTA2	33	5	8.8
Q9vhd7	drosophila	Q9VHD7	33	5	8.8
018916	sus scrofa	018916	33	6	8.8
Q9tsx7	sus scrofa	Q9TSX7	33	6	8.8
Q95m05	bos taurus	Q95M05	33	6	8.8
Q8MGU2	bos taurus	Q8MGU2	33	7	8.8
Q8SNF0	gallinago m	Q8SNF0	33	7	8.8
Q9bac6	euglena gra	Q9BAC6	33	8	8.8
Q8W9G0	meloidogyne	Q8W9G0	33	8	8.8
Q9bacl	euglena ste	Q9BACL	33	8	8.8
Q9xnp3	boophilus m	Q9XNP3	33	8	8.8
078857	phytophthora	078857	33	8	8.8
Q9t2n1	nicotiana t	Q9T2N1	33	8	8.8
Q9bac4	euglena mut	Q9BAC4	33	8	8.8
Q8WEJ5	ginkgo bilo	Q8WEJ5	33	8	8.8
Q8HMH3	chlamydomon	Q8HMH3	33	8	8.8
Q8HS33	hydrastis c	Q8HS33	33	8	8.8
Q38588	bacteriopha	Q38588	33	9	8.8
Q38551	bacteriopha	Q38551	33	9	8.8
049775	arabidopsis	049775	33	10	8.8
Q9S8V5	zea mays (m	Q9S8V5	33	10	8.8
Q90085	human papil	Q90085	33	12	8.8
Q91J04	tt virus. o	Q91J04	33	12	8.8
072996	hepatitis c	072996	33	12	8.8
Q91J14	tt virus. o	Q91J14	33	12	8.8
Q91J12	tt virus. o	Q91J12	33	12	8.8
Q91J15	tt virus. o	Q91J15	33	12	8.8
Q91J07	tt virus. o	Q91J07	33	12	8.8
072995	hepatitis c	072995	33	12	8.8
Q91J09	tt virus. o	Q91J09	33	12	8.8
Q86912	hepatitis c	Q86912	33	12	8.8
Q8VSG7	hepatitis c	Q8VSG7	33	12	8.8
Q91J08	tt virus. o	Q91J08	33	12	8.8
072997	hepatitis c	072997	33	12	8.8
Q83963	avian influ	Q83963	33	12	8.8
Q91J06	tt virus. o	Q91J06	33	12	8.8
072999	hepatitis c	072999	33	12	8.8
Q91J16	tt virus. o	Q91J16	33	12	8.8
072998	hepatitis c	072998	33	12	8.8
Q91J11	tt virus. o	Q91J11	33	12	8.8
072994	hepatitis c	072994	33	12	8.8
Q8V5H0	hepatitis c	Q8V5H0	33	12	8.8
Q91J13	tt virus. o	Q91J13	33	12	8.8
Q8V5G8	hepatitis c	Q8V5G8	33	12	8.8

628	3	8.8	33	12	073007	hepatitis c
629	3	8.8	33	12	091J10	tc virus. o
630	3	8.8	33	12	091J17	tc virus. o
631	3	8.8	33	12	069461	human herpe
632	3	8.8	33	12	08V5G9	hepatitis c
633	3	8.8	33	12	073004	hepatitis c
634	3	8.8	33	12	099138	avian influ
635	3	8.8	33	13	P82740	rana tempor
636	3	8.8	33	13	P82236	rana tempor
637	3	8.8	33	15	Q86107	stman sarc
638	3	8.8	33	16	Q9PA23	xylolla fas
639	3	8.8	33	16	Q9KML1	vibri o choi
640	3	8.8	33	16	Q97T91	streptococc
641	3	8.8	33	16	Q97PC1	streptococc
642	3	8.8	33	16	Q932N2	staphylococ
643	3	8.8	33	16	Q8ZKL2	salmonella
644	3	8.8	33	16	Q8Z1V4	salmonella
645	3	8.8	33	16	Q8XAJ9	eschcherichia
646	3	8.8	33	16	Q8U5M4	agrobacteri
647	3	8.8	33	16	Q8NUL1	staphylococ
648	3	8.8	33	16	Q8KG99	chlorobium
649	3	8.8	33	16	Q8KEJ7	chlorobium
650	3	8.8	33	16	Q8FZ67	brucella su
651	3	8.8	33	16	Q8FYR6	brucella su
652	3	8.8	33	16	Q8FY86	brucella su
653	3	8.8	33	16	Q8EJH6	shewanella
654	3	8.8	33	16	Q8EJ76	shewanella
655	3	8.8	33	16	Q8EGA9	shewanella
656	3	8.8	33	16	Q8EE59	shewanella
657	3	8.8	33	16	Q8EE42	shewanella
658	3	8.8	33	16	Q8E8W4	shewanella
659	3	8.8	33	16	Q8E1Y5	streptococc
660	3	8.8	33	16	Q8DWM3	streptococc
661	3	8.8	33	16	Q8CQY7	staphylococ
662	3	8.8	33	17	Q9HSX6	halobacteri
663	3	8.8	33	17	Q8U2X8	pyrococcus
664	3	8.8	34	2	Q54427	spiroplasma
665	3	8.8	34	2	Q9X3L6	prochiloro
666	3	8.8	34	2	Q9R5U1	campylobact
667	3	8.8	34	2	Q56234	thermus aqu
668	3	8.8	34	2	Q44208	pseudomonas
669	3	8.8	34	2	Q9X7J6	pseudomonas
670	3	8.8	34	2	Q31061	butyrivibri
671	3	8.8	34	2	Q9R8A2	chlamydia t
672	3	8.8	34	2	Q8GJC8	campylobact
673	3	8.8	34	2	Q8G8C9	pseudomonas
674	3	8.8	34	3	Q00377	coccidioid
675	3	8.8	34	4	Q99910	homo sapien
676	3	8.8	34	4	Q9UQN9	homo sapien
677	3	8.8	34	4	Q9H3R8	homo sapien
678	3	8.8	34	4	Q9UI64	homo sapien
679	3	8.8	34	4	Q8WWS1	homo sapien
680	3	8.8	34	4	Q9HBG1	homo sapien
681	3	8.8	34	4	Q9BSP7	homo sapien
682	3	8.8	34	4	Q9H4L8	homo sapien
683	3	8.8	34	4	Q8NEQ3	homo sapien
684	3	8.8	34	4	Q15251	homo sapien

Q9nqy9	homo sapien	34	4	Q9NÖY9	8.8	3	685
Q9bip7	cooperia pu	34	5	Q9BIP7	8.8	3	686
Q9gqes	branchiosto	34	5	Q9GQES	8.8	3	687
Q8n063	plasmodium	34	5	Q8N063	8.8	3	688
Q8itd9	schistosoma	34	5	Q8ITD9	8.8	3	689
F79429	capra hircu	34	6	F79429	8.8	3	690
F82908	bos taurus	34	6	F82908	8.8	3	691
079025	enallagma v	34	8	079025	8.8	3	692
Q8mca2	phaseolus a	34	8	Q8MCA2	8.8	3	693
Q8hkel	rhinicephal	34	8	Q8HKE1	8.8	3	694
Q8w2h0	paspalum no	34	10	Q8W2H0	8.8	3	695
Q8vwl0	paspalum no	34	10	Q8VWL0	8.8	3	696
Q9sca3	lycopersico	34	10	Q9SCA3	8.8	3	697
Q923Z1	mus musculu	34	11	Q923Z1	8.8	3	698
Q8r557	mus musculu	34	11	Q8R557	8.8	3	699
Q9et72	mus musculu	34	11	Q9ET72	8.8	3	700
Q99kx7	mus musculu	34	11	Q99KX7	8.8	3	701
Q64170	mus sp. b-r	34	11	Q64170	8.8	3	702
Q8vhl4	rattus norv	34	11	Q8VHL4	8.8	3	703
Q9dw68	rat cytomeg	34	12	Q9DW68	8.8	3	704
042521	scylliorhinu	34	13	042521	8.8	3	705
013101	ambystoma m	34	13	013101	8.8	3	706
Q8q9g2	oncorhynch	34	13	Q8Q9G2	8.8	3	707
Q8qfM9	oncorhynch	34	13	Q8QFM9	8.8	3	708
042526	scylliorhinu	34	13	042526	8.8	3	709
Q9pre7	oryzias lat	34	13	Q9PRE7	8.8	3	710
Q8q9G1	oncorhynch	34	13	Q8Q9G1	8.8	3	711
Q8QGF7	oncorhynch	34	13	Q8QGF7	8.8	3	712
040445	human immun	34	15	040445	8.8	3	713
Q9wR32	human immun	34	15	Q9WR32	8.8	3	714
Q9w8Y1	chimpanzee	34	15	Q9W8Y1	8.8	3	715
050812	borrelia bu	34	16	050812	8.8	3	716
050877	borrelia bu	34	16	050877	8.8	3	717
Q9pgh3	xylella fas	34	16	Q9PGH3	8.8	3	718
Q9pgf8	xylella fas	34	16	Q9PGF8	8.8	3	719
Q9pfa5	xylella fas	34	16	Q9PFA5	8.8	3	720
Q9pdd0	xylella fas	34	16	Q9PDD0	8.8	3	721
Q9kra8	vibrio chol	34	16	Q9KRA8	8.8	3	722
Q9kpw9	vibrio chol	34	16	Q9KPW9	8.8	3	723
Q9km63	vibrio chol	34	16	Q9KM63	8.8	3	724
Q9k7c6	bacillus ha	34	16	Q9K7C6	8.8	3	725
Q9jy24	neisseria m	34	16	Q9JY24	8.8	3	726
Q9jvp3	neisseria m	34	16	Q9JVP3	8.8	3	727
Q97sf7	streptococc	34	16	Q97SF7	8.8	3	728
Q97p16	streptococc	34	16	Q97P16	8.8	3	729
Q9k2b9	chlamydia p	34	16	Q9K2B9	8.8	3	730
Q8x4v1	escheria	34	16	Q8X4V1	8.8	3	731
Q8u5v2	agrobacteri	34	16	Q8U5V2	8.8	3	732
Q8viy1	mycobacteri	34	16	Q8VIY1	8.8	3	733
Q8ric7	fusobacteri	34	16	Q8RIC7	8.8	3	734
Q8nwx3	staphylococ	34	16	Q8NWX3	8.8	3	735
Q8nwf8	staphylococ	34	16	Q8NWF8	8.8	3	736
Q8nvl0	staphylococ	34	16	Q8NVL0	8.8	3	737
Q8keq8	chlorobium	34	16	Q8KEQ8	8.8	3	738
Q8kel5	chlorobium	34	16	Q8KEL5	8.8	3	739
Q8kde4	chlorobium	34	16	Q8KDE4	8.8	3	740
							741

Q8g2q2 brucella su Q8f897 leptospira Q8f830 leptospira Q8f827 leptospira Q8f5y7 leptospira Q8f0v9 leptospira Q8ezr6 leptospira Q8ez37 leptospira Q8eyw8 leptospira Q8eyg6 leptospira Q8exh6 leptospira Q8exa8 leptospira Q8ej65 shewanella Q8ei45 shewanella Q8ehu5 shewanella Q8ehy3 shewanella Q8ehw3 shewanella Q8el73 streptococ Q8cry3 staphylococ Q8u111 pyrococcus Q9r624 bacillus su Q9r625 bacillus su Q9x3d6 prochloroco Q9r5i3 thermoaer Q9fcx4 clostridium Q9xbk0 bacillus ce Q53564 neisseria g Q46537 bacteroides Q9zg35 chlamydia t Q9rhg5 bacillus ce Q9r4a1 klebsiella Q8rk93 clostridium Q8rk93 clostridium Q8r1w2 clostridium Q9r626 bacillus su P81927 lactobacill Q8gkz7 borrelia bu Q9vut3 saccharomyc Q9bvr9 homo sapien Q13380 homo sapien Q13165 homo sapien Q96fg7 homo sapien Q13828 homo sapien Q13264 homo sapien Q9y634 homo sapien Q9bu09 homo sapien Q8iu77 homo sapien Q9u780 boophilus a Q26372 tritolum c Q9bn11 mesobuthus Q9u782 boophilus m Q9tVj7 boophilus m Q9u783 boophilus m Q9u784 boophilus m Q9u781 boophilus m Q8if21 trypanosoma Q95n74 equus cabal

Q8G2Q2 34 16 Q8F830 34 16 Q8F897 34 16 Q8F827 34 16 Q8F5Y7 34 16 Q8F0V9 34 16 Q8EZR6 34 16 Q8EZ37 34 16 Q8EYW8 34 16 Q8EYG6 34 16 Q8EXH6 34 16 Q8EXA8 34 16 Q8EJ65 34 16 Q8EI45 34 16 Q8EHU5 34 16 Q8E8Y3 34 16 Q8E8W3 34 16 Q8E173 34 16 Q8CRY3 34 16 Q8U111 34 17 Q9R624 35 2 Q9JPG9 35 2 Q9R625 35 2 Q9X3D6 35 2 Q9R5I3 35 2 Q9FCX4 35 2 Q9XBK0 35 2 Q53564 35 2 Q46537 35 2 Q9ZG35 35 2 Q9RHG5 35 2 Q9R4A1 35 2 Q8RK93 35 2 Q8RIW2 35 2 Q9R626 35 2 P81927 35 2 Q8GKZ7 35 2 Q96UT3 35 3 Q9BVR9 35 4 Q13380 35 4 Q13165 35 4 Q96FG7 35 4 Q13828 35 4 Q13264 35 4 Q9Y634 35 4 Q9BU09 35 4 Q8IU77 35 4 Q9U780 35 5 Q26372 35 5 Q9BN11 35 5 Q9U782 35 5 Q9TVJ7 35 5 Q9U783 35 5 Q9U784 35 5 Q9U781 35 5 Q8IF21 35 5 Q95N74 35 6

799	Q9MZA7	6	35	8.8
800	Q951Q6	8	35	8.8
801	Q8W7S9	8	35	8.8
802	Q9GF85	8	35	8.8
803	Q8W7T0	8	35	8.8
804	Q8W7S8	8	35	8.8
805	Q8WE70	8	35	8.8
806	Q8W7S7	8	35	8.8
807	Q9GFP8	8	35	8.8
808	Q94P82	8	35	8.8
809	Q8WEJ7	8	35	8.8
810	Q951S7	8	35	8.8
811	Q951R1	8	35	8.8
812	Q951S1	8	35	8.8
813	Q8WII3	8	35	8.8
814	Q951R3	8	35	8.8
815	Q8WIH9	8	35	8.8
816	Q8WIH5	8	35	8.8
817	Q951S9	8	35	8.8
818	Q8WIII	8	35	8.8
819	Q951Q9	8	35	8.8
820	Q951S4	8	35	8.8
821	Q951R5	8	35	8.8
822	Q9SPU2	10	35	8.8
823	Q9MAB1	10	35	8.8
824	Q9ZUM2	10	35	8.8
825	Q9S9G9	10	35	8.8
826	P92971	10	35	8.8
827	Q9LV08	10	35	8.8
828	Q9IQ64	10	35	8.8
829	Q39297	10	35	8.8
830	Q8RVJ7	10	35	8.8
831	Q9FJ84	10	35	8.8
832	Q8GXK4	10	35	8.8
833	Q63397	11	35	8.8
834	Q9JLA4	11	35	8.8
835	Q60608	11	35	8.8
836	Q9QV30	11	35	8.8
837	Q9QUU2	11	35	8.8
838	Q922H5	11	35	8.8
839	Q99JI5	11	35	8.8
840	Q8BK89	11	35	8.8
841	Q9O151	12	35	8.8
842	Q65380	12	35	8.8
843	Q83333	12	35	8.8
844	O55549	12	35	8.8
845	Q8BB50	12	35	8.8
846	Q90XB5	13	35	8.8
847	P83224	13	35	8.8
848	P83225	13	35	8.8
849	P83227	13	35	8.8
850	P83228	13	35	8.8
851	P83229	13	35	8.8
852	P83226	13	35	8.8
853	Q75981	15	35	8.8
854	Q9J3S2	15	35	8.8
855	Q71950	15	35	8.8

856	3	8.8	35	15	Q91PY2	human immun
857	3	8.8	35	15	Q80574	human immun
858	3	8.8	35	15	Q80601	human immun
859	3	8.8	35	15	Q8QDX6	human immun
860	3	8.8	35	15	Q9QFA0	human immun
861	3	8.8	35	15	Q9YM80	human immun
862	3	8.8	35	15	Q8QDY0	human immun
863	3	8.8	35	15	Q75970	human immun
864	3	8.8	35	15	Q9YM96	human immun
865	3	8.8	35	15	Q9YM22	human immun
866	3	8.8	35	15	Q75990	human immun
867	3	8.8	35	15	Q75989	human immun
868	3	8.8	35	15	Q9YM67	human immun
869	3	8.8	35	15	Q77250	human immun
870	3	8.8	35	15	Q75955	human immun
871	3	8.8	35	15	Q9YM95	human immun
872	3	8.8	35	15	Q91PY4	human immun
873	3	8.8	35	16	007593	bacillus su
874	3	8.8	35	16	Q9KR18	vibrio chol
875	3	8.8	35	16	Q9KNU1	vibrio chol
876	3	8.8	35	16	Q9JWX5	neisseria m
877	3	8.8	35	16	Q9JVB3	neisseria m
878	3	8.8	35	16	Q9A427	caulobacter
879	3	8.8	35	16	Q97T30	streptococc
880	3	8.8	35	16	Q9K241	chlamydia p
881	3	8.8	35	16	Q8XZB7	ralstonia s
882	3	8.8	35	16	Q8X4F4	escherichia
883	3	8.8	35	16	Q8KCA6	chlorobium
884	3	8.8	35	16	Q8G2D4	brucella su
885	3	8.8	35	16	Q8F9H5	leptospira
886	3	8.8	35	16	Q8F8D4	leptospira
887	3	8.8	35	16	Q8F1W8	leptospira
888	3	8.8	35	16	Q8EYH6	leptospira
889	3	8.8	35	16	Q8EGT2	shewanella
890	3	8.8	35	16	Q8EGC0	shewanella
891	3	8.8	35	16	Q8EG97	shewanella
892	3	8.8	35	16	Q8EEP3	shewanella
893	3	8.8	35	16	Q8E9Z1	shewanella
894	3	8.8	35	16	Q8DUY1	streptococc
895	3	8.8	35	17	Q9HMP1	halobacteri
896	3	8.8	35	17	Q8ZXX9	pyrobaculum
897	3	8.8	36	2	006954	salmoneila
898	3	8.8	36	2	Q8VTS7	listeria in
899	3	8.8	36	2	Q9ZG79	chlamydia t
900	3	8.8	36	2	Q9RHE3	pediococcus
901	3	8.8	36	2	Q8VTS5	listeria we
902	3	8.8	36	2	Q44337	agrobacteri
903	3	8.8	36	2	Q9LBB5	helicobacte
904	3	8.8	36	2	Q48507	lactococcus
905	3	8.8	36	2	Q99094	salmoneila
906	3	8.8	36	2	Q9S635	prochloroco
907	3	8.8	36	2	Q8VTR8	listeria iv
908	3	8.8	36	2	Q8VTS0	listeria mo
909	3	8.8	36	2	Q8KYW1	uncultured
910	3	8.8	36	2	Q56028	salmoneila
911	3	8.8	36	2	Q9R4X9	azotobacter
912	3	8.8	36	2	Q9X3G2	prochloroco

913	086086	2	36	8.8	3
914	Q9R536	2	36	8.8	3
915	Q8GRH1	2	36	8.8	3
916	Q96W36	3	36	8.8	3
917	Q9UNV7	4	36	8.8	3
918	Q9PIE9	4	36	8.8	3
919	Q9UPB7	4	36	8.8	3
920	Q9UML4	4	36	8.8	3
921	Q8NE47	4	36	8.8	3
922	Q9GSY9	5	36	8.8	3
923	Q9NGN1	5	36	8.8	3
924	Q27730	5	36	8.8	3
925	Q9GNP3	5	36	8.8	3
926	001333	5	36	8.8	3
927	Q25781	5	36	8.8	3
928	Q8ISR7	5	36	8.8	3
929	Q97889	6	36	8.8	3
930	Q29059	6	36	8.8	3
931	Q9XT44	6	36	8.8	3
932	Q9N1C5	6	36	8.8	3
933	Q97890	6	36	8.8	3
934	P79428	6	36	8.8	3
935	063675	8	36	8.8	3
936	Q9GF81	8	36	8.8	3
937	Q9TIE4	8	36	8.8	3
938	Q9TIF1	8	36	8.8	3
939	Q9GFA3	8	36	8.8	3
940	Q9GF97	8	36	8.8	3
941	Q94VL4	8	36	8.8	3
942	Q36303	8	36	8.8	3
943	Q9TIF0	8	36	8.8	3
944	Q94NY5	8	36	8.8	3
945	Q9GFW6	8	36	8.8	3
946	Q9MSP9	8	36	8.8	3
947	Q9TIF3	8	36	8.8	3
948	Q9GF74	8	36	8.8	3
949	Q9TIE2	8	36	8.8	3
950	Q9TIF2	8	36	8.8	3
951	Q9GF89	8	36	8.8	3
952	Q9MSR0	8	36	8.8	3
953	063650	8	36	8.8	3
954	Q9TIE3	8	36	8.8	3
955	Q9TIE5	8	36	8.8	3
956	Q9GFA9	8	36	8.8	3
957	Q8HS50	8	36	8.8	3
958	Q8HS46	8	36	8.8	3
959	Q8HS42	8	36	8.8	3
960	Q8HS31	8	36	8.8	3
961	Q8HS27	8	36	8.8	3
962	Q8HS18	8	36	8.8	3
963	Q8HKF5	8	36	8.8	3
964	Q8HKC6	8	36	8.8	3
965	Q38977	10	36	8.8	3
966	Q8VY71	10	36	8.8	3
967	Q42097	10	36	8.8	3
968	Q9JMC0	11	36	8.8	3
969	Q60937	11	36	8.8	3
086086	shewanella				
09536	sphingomona				
Q8GRH1	pectobacter				
Q96W36	ophiostoma				
Q9UNV7	homo sapien				
Q9PIE9	homo sapien				
Q9UPB7	homo sapien				
Q9UML4	homo sapien				
Q8NE47	homo sapien				
Q9GSY9	carcinus ma				
Q9NGN1	strongyloce				
Q27730	plasmodium				
Q9GNP3	caenorhabdi				
001333	caenorhabdi				
Q25781	plasmodium				
Q8ISR7	spodoptera				
Q97889	pongo pygma				
Q29059	sus scrofa				
Q9XT44	pongo pygma				
Q9N1C5	bos taurus				
Q97890	pan troglod				
P79428	capra hircu				
063675	emberiza pu				
Q9GF81	gnetum gnem				
Q9TIE4	hydrocotyle				
Q9TIF1	bolax gumm				
Q9GFA3	cabomba car				
Q9GF97	ceratophyl				
Q94VL4	salmo trutt				
Q36303	musa schizo				
Q9TIF0	klotschia				
Q94NY5	salmo salar				
Q9GFW6	lactoris fe				
Q9MSP9	nymphaea od				
Q9TIF3	eremocharis				
Q9GF74	liriodendro				
Q9TIE2	aralia chin				
Q9TIF2	azorella tr				
Q9GF89	drimys wint				
Q9MSR0	zamia furtu				
063650	emberiza sc				
Q9TIE3	hydrocotyle				
Q9TIE5	xanthosia a				
Q9GFA9	acorus cala				
Q8HS50	ascarina lu				
Q8HS46	austrobaile				
Q8HS42	chloranthus				
Q8HS31	lilium supe				
Q8HS27	magnolia st				
Q8HS18	sagittaria				
Q8HKF5	rhidicaphal				
Q8HKC6	haemaphysal				
Q38977	arabidopsis				
Q8VY71	arabidopsis				
Q42097	arabidopsis				
Q9JMC0	ratus norv				
Q60937	mus musculu				

P97598	rattus norv	11	36	8.8	3	970
Q91x80	hepatitis b	12	36	8.8	3	971
Q9qgs6	tanapox vir	12	36	8.8	3	972
Q91x82	hepatitis b	12	36	8.8	3	973
Q90722	calicivirus	12	36	8.8	3	974
Q83609	myxoma viru	12	36	8.8	3	975
Q91cy3	tt virus. o	12	36	8.8	3	976
Q8gqz2	simian viru	12	36	8.8	3	977
Q42264	xenopus lae	13	36	8.8	3	978
Q9w695	gallus gall	13	36	8.8	3	979
Q8ggs0	gallus gall	13	36	8.8	3	980
Q76587	human immun	15	36	8.8	3	981
Q80551	human immun	15	36	8.8	3	982
Q9ynx9	human immun	15	36	8.8	3	983
Q80550	human immun	15	36	8.8	3	984
Q80553	human immun	15	36	8.8	3	985
Q40258	human immun	15	36	8.8	3	986
Q77664	human immun	15	36	8.8	3	987
Q25389	helicobacte	16	36	8.8	3	988
Q50679	borrelia bu	16	36	8.8	3	989
Q50686	borrelia bu	16	36	8.8	3	990
Q50969	borrelia bu	16	36	8.8	3	991
Q9ktv5	vibrio chol	16	36	8.8	3	992
Q9kxb3	vibrio chol	16	36	8.8	3	993
Q9kq34	vibrio chol	16	36	8.8	3	994
Q9kpr2	vibrio chol	16	36	8.8	3	995
Q9kpg3	vibrio chol	16	36	8.8	3	996
Q9klw9	vibrio chol	16	36	8.8	3	997
Q9k7g3	bacillus ha	16	36	8.8	3	998
Q9jtw3	neisseria m	16	36	8.8	3	999
Q8zlt4	salmonella	16	36	8.8	3	1000

ALIGNMENTS

RESULT 1

Q91Y90 ID Q91Y90 PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382953; AAK63072.1; -
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthythorm_sub.

DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidae; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence."
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1
 FT NON_TER 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;
 Query Match 14.7%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 LRKKL 28
 DB 15 LRKKL 19
 RESULT 4
 Q97K50
 ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitt J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum."

RESULT 5
ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angvine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE007622; AAK79045.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 14.7%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVSEI 5
DB 30 SVSEI 34
RESULT 6
ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angvine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 14.7%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 LRKLT 28
DB 26 LRKLT 30
RESULT 6
ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9

DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK011220; BAC25325.1; -
 SQ SEQUENCE 35 AA; 3967 MW; F811566686390ECD8 CRC64;
 Query Match 14.7%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEI 5
 DB 2 SVSEI 6
 RESULT 7
 ID Q97RG6 PRELIMINARY; PRT; 35 AA.
 AC Q97RG6;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0853.
 GN SP0853.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tetelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506 (2001).

DR EMBL; AE007391; AAK74982.1; -
 DR TIGR; SP0853; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;
 Query Match 14.7%; Score 5; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQD 30
 |||||
 DB 30 KKLQD 34

RESULT 8

ID 024285 PRELIMINARY; PRT; 28 AA.
 AC 024285;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LFY protein (Fragment).
 GN LFY.
 OS Pinus radiata (Monterey pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vegetative;
 RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
 RT "Partial characterization of Pinus radiata meristem identity homolog
 gene (LFY).";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U66725; AAB06792.1; -
 FT NON_TER 1
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4BE74 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LKK 27
 |||||
 DB 15 LKK 18

RESULT 9

ID Q49148 PRELIMINARY; PRT; 29 AA.
 AC Q49148;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PQQ biosynthesis polypeptide.
 GN PQQ.

OS Methyllobacterium extorquens.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Methyllobacteriaceae; Methyllobacterium.
 OX NCBI_TaxID=408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AM1;
 RX MEDLINE=94179111; PubMed=8132470;
 RA Morris C.J., Biville F., Turin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthy R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of Methyllobacterium extorquens AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqd, pqg, and pqc.";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;
 Query Match 11.8%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSEI 5
 DB 8 VSEI 11
 RESULT 10
 ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
 AC Q9UCL2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Renal intestinal-type alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney.";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatse.
 DR ProDom; PD001868; Alk_phosphatse; 1.
 SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BBEAD8D0 CRC64;
 Query Match 11.8%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 KKLQ 29
 DB 23 KKLQ 26

RESULT 11

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.

AC Q25603;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Tubulin.

OS Onchocerca volvulus.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

OC Onchocercidae; Onchocerca.

OX NCBI_TaxID=6282;

RN [1]

RP SEQUENCE FROM N.A.

RA Chandrashekar R., Curtis K.C., Weil G.J.;

RT "Onchocerca volvulus cDNA clone.";

RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; U15095; AAA50364.1; -.

SQ SEQUENCE 29 AA; 3539 MW; B917126A923EFF884 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5

DB 4 VSEI 7

RESULT 12

Q9T161

ID Q9T161 PRELIMINARY; PRT; 29 AA.

AC Q9T161;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE Photosystem Q(B) protein (Fragment).

GN PSBA.

OS Allosyncarpia ternata.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucots II; Myrtales; Myrtaceae; Allosyncarpia.

OX NCBI_TaxID=34307;

RN [1]

RP SEQUENCE FROM N.A.

RA Udovitch F., Ladiges P.Y.;

RT "Informativeness of nuclear and chloroplast DNA regions and the

RT phylogeny of the eucalypts and related genera (Myrtaceae).";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF190370; AAF15265.1; -.

KW Chloroplast.

FT NON_TER 1

SQ SEQUENCE 29 AA; 3501 MW; 977D8E6E67E1D833 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VSNF 34
DB 7 VSNF 10

RESULT 13

013043 ID 013043 PRELIMINARY; PRT; 29 AA.
AC 013043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268658; Pubmed=9108066;
RA Schlake T., Schorpp M., Nehls M., Boehm T.;
RT "The nude gene encodes a sequence-specific DNA binding protein with
RT homologs in organisms that lack an anticipatory immune system.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
DR EMBL; Y11539; CAA72302.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR ProDom; PD000425; TF_Fork_head; 1.
FT NON_TER 1
FT NON_TER 29
SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

RESULT 14

Query Match 11.8%; Score 4; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
DB 17 VSEI 20

Q9UBV5 ID Q9UBV5 PRELIMINARY; PRT; 30 AA.
AC Q9UBV5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Intestinal alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi T., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RT Clin. Chem. 38:2539-2542(1992).
DR InterPro; IPR001952; Aik_phosphatse.
DR ProDom; PD001868; Aik_phosphatse; 1.
SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BBEB9BDE6 CRC64;
Query Match 11.8%; Score 4; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 KKLQ 29
DB 24 KKLQ 27
RESULT 15
Q8DZP7
ID Q8DZP7 PRELIMINARY; PRT; 30 AA.
AC Q8DZP7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SAG1053.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tetelin H., Masiagnani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Martini M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AF014240; AAM99934.1; -.
DR TIGR; SAG1053; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 23 KKLQ 26

RESULT 16

Q55314 ID Q55314 PRELIMINARY; PRT; 31 AA.
AC Q55314;

DT 01-NOV-1996 (TRMBLrel. 01, Created)
DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE Urf2 protein (Fragment).
GN URF2.

OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=96085144; PubMed=8521845;
RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate
RT dehydrogenase genes from the thermophilic archaeon Sulfolobus
RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and
RT expression on Escherichia coli.";
RT Eur. J. Biochem. 233:800-808(1995).

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94082761; PubMed=8259927;
RA Arcari P., Russo A.D., Iannicello G., Gallo M., Bocchini V.;
RT "Nucleotide sequence and molecular evolution of the gene coding for
RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
RT archaeobacterium Sulfolobus solfataricus.";

RT Biochem. Genet. 31:241-251(1993).
DR EMBL; X80178; CAA56461.1; -.
FT NON TER 31
SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 WLRK 26
DB 11 WLRK 14

RESULT 17

Q8NEI8 ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
AC Q8NEI8;
DT 01-OCT-2002 (TRMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030993; AAH30993.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;
 Query Match 11.8%; Score 4; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSEI 5
 DB 18 VSEI 21
 RESULT 18
 ID 050669 PRELIMINARY; PRT; 31 AA.
 AC 050669;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BBH11.
 GN BBH11.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid lp28-3.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kervlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Uterback T., Matthey L., McDonald L., Artach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";
 RL Nature 390:580-586(1997).
 DR EMBL; AE000784; AAC66002.1; -.
 DR TIGR; BBH11; -.
 KW Hypothetical protein; Plasmid; Complete proteome.

SEQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;
Query Match 11.8%; Score 4; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 26 KKLQ 29

RESULT 19
Q8EIW8

ID Q8EIW8 PRELIMINARY; PRT; 31 AA.

AC Q8EIW8;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein.

GN S00711.

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Alteromonadaceae; Shewanella.

OX NCBI_TaxID=70863;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MR-1;

RX MEDLINE=22297686; PubMed=12368813;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,

RA Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.,

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

RT Shewanella oneidensis.";

RL Nat. Biotechnol. 20:1118-1123(2002).

DR EMBL; AE015517; AAN53789.1; -.

DR TIGR; S00711; -.

KW Hypothetical protein; Complete proteome.

SEQ SEQUENCE 31 AA; 3597 MW; 7C6C5D55CFF9CFF CRC64;

Query Match 11.8%; Score 4; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHNK 11
DB 1 MHNK 4

RESULT 20

Q9QZQ2

ID Q9QZQ2

PRELIMINARY;

PRT;

32 AA.

AC Q9QZQ2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Neurotensin receptor (Fragment).
 GN NTR OR NTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=99445567; PubMed=10514493;
 RA Tavares D., Tully K., Dobner P.R.;
 RT "Sequences required for induction of neurotensin receptor gene
 RT expression during neuronal differentiation of NIE-115 neuroblastoma
 RT cells.";
 RL J. Biol. Chem. 274:30066-30079(1999).
 DR EMBL; AF172326; AAD51806.1; -.
 DR MGD; MGI:97386; Ntrr.
 KW Receptor.
 FT NON_TER 32
 SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;
 Query Match 11.8%; Score 4; DB 11; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 HLNS 17
 DB 2 HLNS 5
 RESULT 21
 Q9HSZ0
 ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.
 AC Q9HSZ0;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Vng0019h.
 GN VNG0019H.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leitthausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;

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RT "Genome sequence of Halobacterium species NRC-1."
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AF004971; AAG18659.1; -.
KW Complete proteome.
SQ SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64;

Query Match 11.8%; Score 4; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLD 30
DB 13 KLD 16

RESULT 22
ID Q95SD4 PRELIMINARY; PRT; 33 AA.
AC Q95SD4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM02640p.
GN BCDNA:GM02640.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Numoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060847; AAL28395.1; -.
DR FlyBase; FBgn0047288; BCDNA:GM02640.
SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBB4A7 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KLD 29
DB 21 KLD 24

RESULT 23
ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
AC Q9PKX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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Query Match 11.8%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
 Q9ZG81
 ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
 AC Q9ZG81;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE ATP-dependent permease (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF087260; AAD04038.1; -.
 FT NON_TER 1
 FT NON_TER 34
 FT NON_TER 34
 SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Hypothetical protein TC0337.
 GN TC0337.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPN / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
 pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002301; AAF39200.1; -.
 DR TIGR; TC0337; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

QY 24 LRKK 27
 DB 26 LRKK 29

QY 24 LRKK 27
DB 25 LRKK 28

RESULT 25

Q8GFK2
ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
AC Q8GFK2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ORF37.
OS Staphylococcus aureus.
OG plasmid EDINA plasmid.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-1;
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
plasmid.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003089; BAC54529.1; -.
KW plasmid.
SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLO 29
DB 6 KKLO 9

RESULT 26

Q8C4P4
ID Q8C4P4 PRELIMINARY; PRT; 34 AA.
AC Q8C4P4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Zinc finger homeodomain 4 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.
 RL Nature 420:563-573 (2002).
 DR EMBL; AK081561; BAC38260.1; --
 FT NON_TER 1
 SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;
 Query Match 11.8%; Score 4; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLD 30
 DB 2 KLD 5

RESULT 27

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
 AC Q90ZJ4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain long form (Fragment).
 GN PDGF-A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363439; PubMed=11470524;
 RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
 RT "Characterization and expression of three forms of cDNA encoding
 RT chicken platelet-derived growth factor-A chain."
 RL Gene 272:181-190 (2001).
 DR EMBL; AB031024; BAB62544.1; --
 FT NON_TER 1
 SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKL 28
 DB 28 RKL 31

RESULT 28

ID Q98FK5 PRELIMINARY; PRT; 34 AA.
 AC Q98FK5;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein msr3733.

Query Match 11.8%; Score 4; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GN MS3733.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; Pubmed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003002; BAB50562.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 34 AA; 3804 MW; D6AAA82FECB590413 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 KLQD 30
 DB 28 KLQD 31

RESULT 29
 ID Q15421 PRELIMINARY; PRT; 35 AA.
 AC Q15421;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE Stilian sarcoma associated virus (SSAV)-related pol region DNA
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87071681; Pubmed=2431542;
 RA Leib-Mosch C., Brack R., Werner T., Ertle V., Hehlmann R.;
 RT "Isolation of an SSAV-related endogenous sequence from Human DNA.";
 RL Virology 155:666-677(1986).
 DR EMBL; M14911; AAA36592.1; -
 FT NON_TER 1
 FT NON_TER 35
 SQ SEQUENCE 35 AA; 3742 MW; 2F70B02EE0BC86DF CRC64;

QY 28 LQDV 31
DB 6 LQDV 9

RESULT 30

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
AC Q8V6J8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 4.1 kDa protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=33771;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
RT "Sequence and transcription of halovirus HF2."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222060; AAL55025.1; -
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 4115 MW; 2652C319622B9CE4 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSE 4
DB 10 SVSE 13

RESULT 31

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.
AC Q9KQG4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein VC2034.
GN VC2034.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; Pubmed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*

cholerae.";

RT Nature 406:477-483 (2000).

DR EMBL; AF004278; AAF95182.1; -.

DR TIGR; VC2034; -.

KW Hypothetical protein; Complete proteome.

SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

26 KKLQ 29

||||

24 KKLQ 27

DB

RESULT 32

Q8F102

ID Q8F102

PRELIMINARY; PRT; 35 AA.

AC Q8F102;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN LA3339.

OS Leptospira interrogans.

OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.

OX NCBI_TaxID=173;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lat;

RA Ren S.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE011494; AAN50536.1; -.

KW Hypothetical protein; Complete proteome.

SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

14 HLNS 17

||||

3 HLNS 6

DB

RESULT 33

Q53920

ID Q53920

PRELIMINARY; PRT; 36 AA.

AC Q53920;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE OrfA protein (Fragment).

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34
068941
ID 068941 PRELIMINARY; PRT; 36 AA.
AC 068941;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Dinitrogenase 3 beta subunit (Fragment).
GN ANFK.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A.
RA Lovelace T.M., Bishop P.E.;
RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
in Diverse Diazotrophs.";
RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058778; AAC14327.1; -
DR InterPro; IPR000510; Oxred_nitrognasel.
DR Pfam; PF00148; oxidored_nitro; 1.
FT NON_TER 36
SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFPD437D97 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORFA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
of two FK506-binding domains with its gene transcriptionally coupled
to the FKBP-12 gene.";
RT EMBO J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84281.1; -
DR InterPro; IPR004347; DUF245.
DR Pfam; PF03136; DUF245; 1.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4121 MW; EBD470AAAF99A728E CRC64;

QY 24 LRKK 27
DB 5 LRKK 8

RESULT 35

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.

AC Q8WXW8; 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Urea transporter JK glycoprotein (Fragment).
GN JK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;
RT "Molecular Basis of the JK(a-b-) Phenotype in Non-Finnish European
RT Pedigrees.";
RL Br. J. Haematol. 0:0-0(2001).
DR EMBL; AF328890; AAL37474.1; -.
DR InterPro; IPR004937; Urea_transporter.
DR Pfam; PF03253; UT; 1.
FT NON_TER 1
SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNSM 18
DB 7 LNSM 10

RESULT 36

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.

AC Q9SJ63; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE At2g35870 protein.
GN AT2G35870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; Pubmed=10617197;

Query Match 11.8%; Score 4; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 4 KKLQ 7

RESULT 37

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Greasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eissen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.,
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RT Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007017; AAD21470.1; -
SQ SEQUENCE 36 AA; 4358 MW; DC966779BBDB6B834 CRC64;

ID Q9PXD1 PRELIMINARY; PRT; 36 AA.
AC Q9PXD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Genome polypeptide [Contains: envelope glycoprotein E2/NS1 (GP68)]
DE (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343121; PubMed=8750162;
RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.,
RT "Genotype, slow decrease in virus titer during interferon treatment
and high degree of sequence variability of hypervariable region are
indicative of poor response to interferon treatment in patients with
chronic hepatitis type C.";
RL J. Hepatol. 23:648-653(1995).
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KM Polypeptide; Transmembrane.
SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.7e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8
DB 33 IQLM 36

RESULT 38

ID Q91D77 PRELIMINARY; PRT; 36 AA.
AC Q91D77;

DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE ORF2 hypothetical protein, isolate:HM0319 (Fragment).

OS TTV-like mini virus.
OC Viruses; ssDNA viruses; Circoviridae.

OX NCBI_TaxID=93678;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=HM0319;

RA Michitaka K., Matsubara H., Horike N., Kihana T., Yano M., Mori T.,
RA Onji M.;

RT "Existence of TT virus DNA and TTV-like mini virus DNA in infant cord
RT blood.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB059561; BAB69654.1; -

DR InterPro: IPR004118; TT_ORF2.
DR Pfam: PF02957; TT_ORF2; 1.

KW Hypothetical protein.
FT NON TER 36

SQ SEQUENCE 36 AA; 4291 MW; 92145F475EA841F1 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 14 KKLQ 17

RESULT 39

ID Q9YHT9 PRELIMINARY; PRT; 36 AA.
AC Q9YHT9;

DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Synaposome-associated protein 25.2 (Fragment).

GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99057281; PubMed=9843147;
 RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Larhammar D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage.";
 RL J. Neurosci. Res. 54:563-573(1998).
 DR EMBL; AF091596; AAC73006.1; -.
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 FT NON_TER 1
 FT NON_TER 36
 SEQUENCE 36 AA; 4046 MW; E3434855F7BEC02F CRC64;
 Query Match 11.8%; Score 4; DB 13; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 ERVE 22
 DB 2 ERVE 5
 RESULT 40
 Q97S91
 ID Q97S91 PRELIMINARY; PRT; 36 AA.
 AC Q97S91;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0497.
 GN SP0497.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).
 DR EMBL; AE007361; AAK74655.1; -.
 DR TIGR; SP0497; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 36 AA; 4282 MW; 749D427D078ACA76 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
 ||||
 DB 10 KKLQ 13

Search completed: January 14, 2004, 10:41:52
 Job time : 27.4206 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 5.61371 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-163

Perfect score: 34

Sequence: 1 SVSEIQLMHNNKGKHLNLSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
1	5	14.7	33	1	FABI RHASA	P81175 rhamdia sap
2	4	11.8	29	1	DMD RAT	P11530 rattus norv
3	4	11.8	30	1	PCG3_PACGO	P82416 pachycondyl
4	4	11.8	39	1	PSBY_SYNY3	P73676 synechocyst
5	4	11.8	39	1	SRIC_SARPE	P08377 sarcophaga
6	3	8.8	28	1	CH60_MYCSM	P80673 mycobacteri
7	3	8.8	28	1	COXB_SOLTU	P80499 solanum tub
8	3	8.8	28	1	GUN_SCHCO	P81190 schizophyll
9	3	8.8	28	1	OMPA_YERPS	P38399 yersinia ps
10	3	8.8	28	1	PA2C_PSEPO	P20260 pseudochis
11	3	8.8	28	1	SCX2_BUTSI	P15230 buthus sind
12	3	8.8	28	1	SLP1_LEIQH	P80669 leirus qui
13	3	8.8	28	1	VIP_ALIMI	P48142 alligator m
14	3	8.8	28	1	VIP_RANRI	P81016 rana ridibu
15	3	8.8	28	1	VIP_SHEEP	P04565 ovis aries
16	3	8.8	29	1	CXOC_CONMA	P37300 conus magus
17	3	8.8	29	1	GATA_ALIMI	P47215 alligator m

P47214	amia calva	29	1	GALA_AMICA	8.8	3	18
P30802	gallus gall	29	1	GALA_CHICK	8.8	3	19
P47213	oncorhynch	29	1	GALA_ONCMY	8.8	3	20
P47216	rana ridibu	29	1	GALA_RANRI	8.8	3	21
P31234	ovis aries	29	1	GALA_SHEEP	8.8	3	22
P31297	chinchilla	29	1	GLUC_CHIBR	8.8	3	23
P19371	desulfovibr	29	1	IPYR_DESVH	8.8	3	24
P80267	solanum tub	29	1	NUOI_SOLTU	8.8	3	25
P82417	pachycondyl	29	1	PCG4_PACGO	8.8	3	26
O93639	methanosarc	29	1	RS7_METTE	8.8	3	27
P80740	olea europae	29	1	SODC_OLFEU	8.8	3	28
P81834	spiniacia ol	29	1	TL16_SPIOL	8.8	3	29
P81079	desulfuromo	30	1	CY35_DESAC	8.8	3	30
P80279	phyllomedus	30	1	DMS3_PHYSA	8.8	3	31
P28733	bacteroides	30	1	FTN_BACFR	8.8	3	32
P41521	anguilla an	30	1	GLUM_ANGAN	8.8	3	33
P11726	aeromonas p	30	1	OTCC_AERPU	8.8	3	34
P82415	pachycondyl	30	1	PCG2_PACGO	8.8	3	35
P83476	thrixopelma	30	1	TX2_THRPR	8.8	3	36
P82037	uperoletia i	30	1	UP61_UPEIN	8.8	3	37
P82038	uperoletia i	30	1	UP62_UPEIN	8.8	3	38
Q04238	equisetum a	30	1	VAA2_EQUAR	8.8	3	39
O51473	borrelia bu	30	1	Y523_BORBU	8.8	3	40
O46201	drosophila	31	1	A98A_DEOME	8.8	3	41
P14661	sus scrofa	31	1	CEC1_PIG	8.8	3	42
P56708	conus marmo	31	1	CXMA_CONMR	8.8	3	43
P82372	diploptera	31	1	DIUX_DIPPU	8.8	3	44
P15872	tritricum ae	31	1	H13_WHEAT	8.8	3	45
P81052	leuconostoc	31	1	LCCB_LEUME	8.8	3	46
Q53017	buchnera ap	31	1	LPL_BUCRP	8.8	3	47
P41124	photorhabdu	31	1	MALK_PHOJU	8.8	3	48
P19877	homo sapien	31	1	NAP4_HUMAN	8.8	3	49
Q9bbr4	lotus japon	31	1	PETL_LOTJA	8.8	3	50
P12179	marchantia	31	1	PETL_MARPO	8.8	3	51
Q9mun4	mesostigma	31	1	PETL_MESVI	8.8	3	52
Q9tky9	nephroselm	31	1	PETL_NEPOL	8.8	3	53
Q9cqd6	mus musculu	31	1	SARL_MOUSE	8.8	3	54
P42532	oryctolagus	31	1	SARL_RABIT	8.8	3	55
O51762	borrelia bu	31	1	Y822_BORBU	8.8	3	56
P28487	drosophila	32	1	ADHR_DROYA	8.8	3	57
P01264	oncorhynch	32	1	CAL2_ONCKE	8.8	3	58
P01265	oncorhynch	32	1	CAL3_ONCKI	8.8	3	59
P01262	anguilla ja	32	1	CAL_ANGJA	8.8	3	60
O80296	bacterioph	32	1	COA2_BPIFI	8.8	3	61
P81078	desulfuromo	32	1	CY31_DESAC	8.8	3	62
P02343	synecchocyst	32	1	DBH_SYNY1	8.8	3	63
P55224	salmonella	32	1	RF21_SALEN	8.8	3	64
P10293	cucurbita p	32	1	ITR3_CUCPE	8.8	3	65
P07853	cucurbita m	32	1	ITR4_CUCMA	8.8	3	66
P02875	dolichos ax	32	1	LEC_DOLAX	8.8	3	67
O78499	guillardia	32	1	PETM_GUITH	8.8	3	68
P13064	desulfovibr	32	1	PHSS_DESBN	8.8	3	69
P19589	pisum sativ	32	1	PSBQ_PEA	8.8	3	70
P49516	odontella s	32	1	PSBT_ODOSI	8.8	3	71
Q8s189	euglena ste	32	1	PSBZ_EUGST	8.8	3	72
Q8s187	euglena vir	32	1	PSBZ_EUGVI	8.8	3	73
P39247	bacterioph	32	1	Y160_BPT4	8.8	3	74

75	3	8.8	32	1	YCPG_MASIA
76	3	8.8	33	1	GLU2_ORENI
77	3	8.8	33	1	T1F_PARTE
78	3	8.8	33	1	YC12_EUGGR
79	3	8.8	34	1	DMS1_PHYSA
80	3	8.8	34	1	DMS2_PHYSA
81	3	8.8	34	1	GAST_CAPHI
82	3	8.8	34	1	GUNI_SCLSC
83	3	8.8	34	1	TX1_SCOGR
84	3	8.8	35	1	CECA_AEDAL
85	3	8.8	35	1	COPA_CANFA
86	3	8.8	35	1	CP12_PIG
87	3	8.8	35	1	GP58_BPSPI
88	3	8.8	35	1	HCYA_CHEDE
89	3	8.8	35	1	LECI_CYTSE
90	3	8.8	35	1	LEC3_ULFEU
91	3	8.8	35	1	PBP_ORGPS
92	3	8.8	35	1	PETG_CVACA
93	3	8.8	35	1	PSBT_MARPO
94	3	8.8	35	1	RL15_SYNP7
95	3	8.8	35	1	SCCK_TITSE
96	3	8.8	35	1	SCX1_BUTSI
97	3	8.8	35	1	TMTX_MESTA
98	3	8.8	35	1	TX1_GRASPI
99	3	8.8	35	1	TX1_THRPR
100	3	8.8	35	1	TX2_GRASPI
101	3	8.8	35	1	VORB_METTM
102	3	8.8	35	1	Y210_HAEIN
103	3	8.8	35	1	YRKM_BACSU
104	3	8.8	36	1	ELH_THETS
105	3	8.8	36	1	NPF_ARTTR
106	3	8.8	36	1	OSTS_YEAST
107	3	8.8	36	1	PETM_SYNY3
108	3	8.8	36	1	R18A_BOVIN
109	3	8.8	36	1	RET4_CHICK
110	3	8.8	36	1	RL6_HALCU
111	3	8.8	36	1	Y260_BACHD
112	3	8.8	36	1	Y609_ARCFU
113	3	8.8	37	1	DIU1_TENMO
114	3	8.8	37	1	LCCNM_IACIA
115	3	8.8	37	1	PIP7_BOVIN
116	3	8.8	37	1	RK36_ODOSI
117	3	8.8	37	1	RL36_BACSU
118	3	8.8	37	1	RL36_CLOAB
119	3	8.8	37	1	RL36_LISMO
120	3	8.8	37	1	RL36_PASMU
121	3	8.8	37	1	RL36_STYAM
122	3	8.8	37	1	SCKI_MESTA
123	3	8.8	37	1	VGJ_BPPHX
124	3	8.8	37	1	Y63_BPT3
125	3	8.8	38	1	CPRP_CANPG
126	3	8.8	38	1	NLT1_VITXS
127	3	8.8	38	1	NLT2_VITXS
128	3	8.8	38	1	OBP2_HYSCR
129	3	8.8	38	1	PYSA_METBA
130	3	8.8	38	1	RL36_CHLTE
131	3	8.8	38	1	RL36_ECOLI
75	3	8.8	32	1	P29735_mastigoclad
76	3	8.8	33	1	P81027_oreochromis
77	3	8.8	33	1	Q27172_paramectium
78	3	8.8	33	1	P31559_euglena gra
79	3	8.8	34	1	P24302_phyllomedus
80	3	8.8	34	1	P80278_phyllomedus
81	3	8.8	34	1	P04564_capra hircu
82	3	8.8	34	1	P21833_sclerotinia
83	3	8.8	34	1	P56855_scodra gris
84	3	8.8	35	1	P81417_aedes albop
85	3	8.8	35	1	P40765_canis famli
86	3	8.8	35	1	P80736_sus scrofa
87	3	8.8	35	1	O48412_bacterioph
88	3	8.8	35	1	P83173_cherax dest
89	3	8.8	35	1	P22970_cytisus ses
90	3	8.8	35	1	P23032_ulex europe
91	3	8.8	35	1	P34178_orygia pseu
92	3	8.8	35	1	Q9T1q9_cyanidium c
93	3	8.8	35	1	P12182_marchantia
94	3	8.8	35	1	P31160_synochococc
95	3	8.8	35	1	P56219_titius serr
96	3	8.8	35	1	P15229_buthus sind
97	3	8.8	35	1	Q9bn12_mesobuthus
98	3	8.8	35	1	P56852_grammostola
99	3	8.8	35	1	P83480_thrixopelma
100	3	8.8	35	1	P56853_grammostola
101	3	8.8	35	1	P80908_methanobact
102	3	8.8	35	1	P43964_haemophilus
103	3	8.8	35	1	P54440_bacillus su
104	3	8.8	36	1	P80594_theromyzon
105	3	8.8	36	1	P41334_artioposthi
106	3	8.8	36	1	Q99380_saccharomyc
107	3	8.8	36	1	P74810_synochocyst
108	3	8.8	36	1	P82919_bos taurus
109	3	8.8	36	1	P30370_gallus gall
110	3	8.8	36	1	P05968_halobacteri
111	3	8.8	36	1	Q9kg53_bacillus ha
112	3	8.8	36	1	Q29646_archaeoglob
113	3	8.8	37	1	P56618_tenebrio mo
114	3	8.8	37	1	P83002_lactococcus
115	3	8.8	37	1	P21671_bos taurus
116	3	8.8	37	1	P49568_odontella s
117	3	8.8	37	1	P20278_bacillus su
118	3	8.8	37	1	Q97ek2_clostridium
119	3	8.8	37	1	Q927n0_listeria mo
120	3	8.8	37	1	P57942_pasteurella
121	3	8.8	37	1	Q99s42_staphylococ
122	3	8.8	37	1	P24663_mesobuthus
123	3	8.8	37	1	P03651_bacterioph
124	3	8.8	37	1	P20328_bacterioph
125	3	8.8	38	1	P81033_cancer pagu
126	3	8.8	38	1	P80275_vitis sp. (
127	3	8.8	38	1	P33556_vitis sp. (
128	3	8.8	38	1	P81648_hystrix cri
129	3	8.8	38	1	P80521_methanosarc
130	3	8.8	38	1	Q8kaj4_chlorobium
131	3	8.8	38	1	P21194_escherichia

132	3	8.8	38	1	RL36_PSEAE
133	3	8.8	38	1	RL36_THEMEA
134	3	8.8	38	1	RL36_YERPE
135	3	8.8	38	1	RL12_PINCO
136	3	8.8	38	1	SCX8_LEIOH
137	3	8.8	38	1	Y114_HAEIN
138	3	8.8	38	1	YJ39_ARCFU
139	3	8.8	39	1	CEC_GLOMR
140	3	8.8	39	1	COLI_BALPH
141	3	8.8	39	1	COLI_RABIT
142	3	8.8	39	1	COLI_SQUAC
143	3	8.8	39	1	COLI_STRCA
144	3	8.8	39	1	EXE3_HELHO
145	3	8.8	39	1	FUC3_RAT
146	3	8.8	39	1	GVPC_SPICC
147	3	8.8	39	1	H2A_BUFBG
148	3	8.8	39	1	LGGA_LACIA
149	3	8.8	39	1	PSBX_PORPU
150	3	8.8	39	1	SC62_CANFA
151	3	8.8	40	1	ALB1_TRASC
152	3	8.8	40	1	HS9A_RABIT
153	3	8.8	40	1	KAD_STACA
154	3	8.8	40	1	PHRK_BACSU
155	3	8.8	40	1	PRE_BACLI
156	3	8.8	40	1	RK33_PEA
157	3	8.8	40	1	RRPO_LSV
158	3	8.8	40	1	SAUV_PHYSA
159	3	8.8	40	1	SRID_SARPE
160	3	8.8	40	1	VIT_MELGA
161	3	8.8	40	1	YDRB_STRPE
162	2	5.9	28	1	ACON_CANAL
163	2	5.9	28	1	APC1_RABIT
164	2	5.9	28	1	ARYC_NOGGL
165	2	5.9	28	1	CIQC_RAT
166	2	5.9	28	1	ETX2_BACCE
167	2	5.9	28	1	FIBA_CANFA
168	2	5.9	28	1	FLA1_TREPH
169	2	5.9	28	1	GDO_TRIMO
170	2	5.9	28	1	GRP_ATLMI
171	2	5.9	28	1	GTS5_CHICK
172	2	5.9	28	1	GVPC_OSCAG
173	2	5.9	28	1	HORC_HORSP
174	2	5.9	28	1	ICPP_VIPLE
175	2	5.9	28	1	IEL1_MOMCH
176	2	5.9	28	1	IORB_METTM
177	2	5.9	28	1	ITR2_MOMCH
178	2	5.9	28	1	ITR3_LUFVCY
179	2	5.9	28	1	ITRA_MOMCH
180	2	5.9	28	1	LECA_IRIHO
181	2	5.9	28	1	LPFS_ECOLI
182	2	5.9	28	1	LPL_ECOLI
183	2	5.9	28	1	LPL_SALTI
184	2	5.9	28	1	LPL_SALTY
185	2	5.9	28	1	LPW_SERMA
186	2	5.9	28	1	MAAI_RAT
187	2	5.9	28	1	MCDB_MEGPE
188	2	5.9	28	1	NLT2_WHEAT
132	3	8.8	38	1	RL36_PSEAE
133	3	8.8	38	1	RL36_THEMEA
134	3	8.8	38	1	RL36_YERPE
135	3	8.8	38	1	RL12_PINCO
136	3	8.8	38	1	SCX8_LEIOH
137	3	8.8	38	1	Y114_HAEIN
138	3	8.8	38	1	YJ39_ARCFU
139	3	8.8	39	1	CEC_GLOMR
140	3	8.8	39	1	COLI_BALPH
141	3	8.8	39	1	COLI_RABIT
142	3	8.8	39	1	COLI_SQUAC
143	3	8.8	39	1	COLI_STRCA
144	3	8.8	39	1	EXE3_HELHO
145	3	8.8	39	1	FUC3_RAT
146	3	8.8	39	1	GVPC_SPICC
147	3	8.8	39	1	H2A_BUFBG
148	3	8.8	39	1	LGGA_LACIA
149	3	8.8	39	1	PSBX_PORPU
150	3	8.8	39	1	SC62_CANFA
151	3	8.8	40	1	ALB1_TRASC
152	3	8.8	40	1	HS9A_RABIT
153	3	8.8	40	1	KAD_STACA
154	3	8.8	40	1	PHRK_BACSU
155	3	8.8	40	1	PRE_BACLI
156	3	8.8	40	1	RK33_PEA

189	2	5.9	28	1	NXL1_BOUAN	P34074	boulengerin
190	2	5.9	28	1	OBP1_HYSCR	P81647	hystrix cri
191	2	5.9	28	1	ORND_PLAOR	P25513	placobdella
192	2	5.9	28	1	OST1_CHICK	P80896	gallus gall
193	2	5.9	28	1	PA22_MICNI	P21791	micrurus ni
194	2	5.9	28	1	PA23_TRIST	P82894	trimeresuru
195	2	5.9	28	1	PETL_CYAPA	P48102	cyanophora
196	2	5.9	28	1	PHR_METTM	P58818	methanobact
197	2	5.9	28	1	PHYB_ASPFI	P81440	aspergillus
198	2	5.9	28	1	PP71_HCMVT	P24429	human cytom
199	2	5.9	28	1	PPOX_BOVIN	P56602	bos taurus
200	2	5.9	28	1	RL5_HALCU	P05972	halobacteri
201	2	5.9	28	1	RS19_PHYS1	O66093	phytoplasma
202	2	5.9	28	1	SCK2_ORTSC	P83244	orthochirus
203	2	5.9	28	1	SMS2_ORENI	P81029	oreochromis
204	2	5.9	28	1	TXO2_AGEAP	P15971	agelenopsis
205	2	5.9	28	1	VG9_SPV4	P11341	spiroplasma
206	2	5.9	28	1	VIP_DIDMA	P39089	didelphis m
207	2	5.9	28	1	VIP_SCYCA	P09685	scyliorhinu
208	2	5.9	28	1	Y073_ARCFU	O30163	archaeoglob
209	2	5.9	28	1	Y16P_BPT4	P39248	bacterioph
210	2	5.9	28	1	YA79_ARCFU	O29184	archaeoglob
211	2	5.9	29	1	12AH_CLOS4	P21215	clostridium
212	2	5.9	29	1	AL21_HORSE	P81216	equus cabal
213	2	5.9	29	1	AMEL_RABIT	P12761	oryctolagus
214	2	5.9	29	1	ATP9_PICPJ	Q06838	pichia pijp
215	2	5.9	29	1	ATPA_BRYMA	P26965	bryopsis ma
216	2	5.9	29	1	BR2D_RANES	P40840	rana escule
217	2	5.9	29	1	BREE_RANES	P40841	rana escule
218	2	5.9	29	1	CERB_CERCA	P36191	ceratitis c
219	2	5.9	29	1	COA1_BPI22	P15413	bacterioph
220	2	5.9	29	1	COXJ_CANFA	Q9tr29	canis famil
221	2	5.9	29	1	COXK_SHEEP	Q9tr28	ovis aries
222	2	5.9	29	1	CU36_LOCFI	P11737	locusta mig
223	2	5.9	29	1	CXD6_CONGL	Q9twm7	conus glori
224	2	5.9	29	1	CXO7_CONGE	P05483	conus geogr
225	2	5.9	29	1	CXOD_CONMA	Q26350	conus magus
226	2	5.9	29	1	CXST_CONGE	P58844	conus geogr
227	2	5.9	29	1	CYO4_VIOOD	P58436	viola odora
228	2	5.9	29	1	DMS5_PHYSA	P80281	phyllomedus
229	2	5.9	29	1	GLUC_ANAPL	P01276	anas platyr
230	2	5.9	29	1	GLUC_CALMI	P13189	callorhynch
231	2	5.9	29	1	GLUC_DIDMA	P18108	didelphis m
232	2	5.9	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
233	2	5.9	29	1	GLUC_PLAFE	P23062	platichthys
234	2	5.9	29	1	GLUC_RABIT	P25449	oryctolagus
235	2	5.9	29	1	GLUC_TORMA	P09567	torpedo mar
236	2	5.9	29	1	H2B2_ECHES	P13282	echinus esc
237	2	5.9	29	1	HOXY_RHOOP	P22660	rhodococcus
238	2	5.9	29	1	HRJ_BOTJA	P20416	bothrops ja
239	2	5.9	29	1	HS98_NEUCR	P31540	neurospora
240	2	5.9	29	1	ITH3_BOVIN	P56652	bos taurus
241	2	5.9	29	1	ITR1_CUCMA	P01074	cucurbita m
242	2	5.9	29	1	ITR1_LUFCY	P25849	luffa cylin
243	2	5.9	29	1	ITR1_MOMRE	P17680	momordica r
244	2	5.9	29	1	ITR2_BRYDI	P11968	bryonia dio
245	2	5.9	29	1	ITR3_CYCPE	P83394	cyclanthera

246	2	5.9	29	1	ITR4_CYCPE	P83395	cyclanthera
247	2	5.9	29	1	ITR5_CYCPE	P83396	cyclanthera
248	2	5.9	29	1	MDH_BURPS	P80536	burkholderi
249	2	5.9	29	1	MULR_ECHML	P81798	echis multi
250	2	5.9	29	1	PETN_ANASP	Q913p6	anabaena sp
251	2	5.9	29	1	PETN_ARATH	P12178	arabidopsis
252	2	5.9	29	1	PETN_CHAGL	Q8ma13	chaetosphae
253	2	5.9	29	1	PETN_CYAPA	P48258	cyanophora
254	2	5.9	29	1	PETN_GUIITH	O78498	guillardia
255	2	5.9	29	1	PETN_MAIZE	Q33302	zea mays (m
256	2	5.9	29	1	PETN_MARPO	P12177	marchantia
257	2	5.9	29	1	PETN_MESVI	Q9mus4	mesostigma
258	2	5.9	29	1	PETN_ODOSI	P49527	odontella s
259	2	5.9	29	1	PETN_PINTH	P41611	pinus thunb
260	2	5.9	29	1	PETN_PORPU	P51276	porphyra pu
261	2	5.9	29	1	PETN_PSINU	Q8wi23	psilotum nu
262	2	5.9	29	1	PETN_SYNEL	Q8dkn2	synechococc
263	2	5.9	29	1	PETN_SYNY3	P72717	synechocyst
264	2	5.9	29	1	PK4_DICDI	P34103	dictyosteli
265	2	5.9	29	1	PRO1_DACGL	P18689	dactylis gl
266	2	5.9	29	1	PSAF_SYNP6	P31083	synechococc
267	2	5.9	29	1	PSAK_SPIOL	P14627	spinacia ol
268	2	5.9	29	1	PSAX_SYNVU	P23320	synechococc
269	2	5.9	29	1	PSBI_SYNVU	P12240	synechococc
270	2	5.9	29	1	RL15_HALCU	P05971	halobacteri
271	2	5.9	29	1	RL15_STRLI	P49975	streptomyce
272	2	5.9	29	1	RP54_CLOKL	P38944	clostridium
273	2	5.9	29	1	SCX1_ANDMA	P56215	androctonus
274	2	5.9	29	1	SDHB_CLOPR	P80213	clostridium
275	2	5.9	29	1	SLP2_LEIQH	P80670	leiurus qui
276	2	5.9	29	1	SLP3_LEIQH	P80671	leiurus qui
277	2	5.9	29	1	TAT_HV1Z3	P12510	human immun
278	2	5.9	29	1	TLP_ACTDE	P81370	actinidia d
279	2	5.9	29	1	UN23_CLOPA	P81356	clostridium
280	2	5.9	29	1	Y15_BPT7	P03792	bacterioph
281	2	5.9	29	1	Y51_BPT3	P20326	bacterioph
282	2	5.9	29	1	YCX4_ODOSI	P49830	odontella s
283	2	5.9	29	1	YXCX_ODOSI	P49838	odontella s
284	2	5.9	30	1	2ENR_CLOTY	P11887	clostridium
285	2	5.9	30	1	A1AT_CHIVI	P38026	chinchilla
286	2	5.9	30	1	AATC_RABIT	P12343	oryctolagus
287	2	5.9	30	1	AATM_RABIT	P12345	oryctolagus
288	2	5.9	30	1	ACB1_DIGLA	P81624	digitalis l
289	2	5.9	30	1	AMPT_BACST	P00728	bacillus st
290	2	5.9	30	1	ANF_RANRI	P09196	rana ridibu
291	2	5.9	30	1	CALM_LYTPI	P05935	lytechinus
292	2	5.9	30	1	CBAL_BACST	P13722	bacillus st
293	2	5.9	30	1	CH60_CLOPA	P81339	clostridium
294	2	5.9	30	1	CIRA_CHAPA	P56871	chassalia p
295	2	5.9	30	1	CLPA_PINPS	P81671	pinus pinas
296	2	5.9	30	1	COAE_CORAM	P58101	corynebacte
297	2	5.9	30	1	COXC_SOLTU	P80500	solanum tub
298	2	5.9	30	1	CRG2_SCOWA	P19865	scoliodon w
299	2	5.9	30	1	CX2A_CONBE	P58625	conus betul
300	2	5.9	30	1	CX7A_CONTU	P58923	conus tulip
301	2	5.9	30	1	CXEX_CONCN	P58928	conus conso
302	2	5.9	30	1	CXK4_CONST	P58921	conus stria

303	2	5.9	30	1	CXOB_CONPE	P56713	conus penna
304	2	5.9	30	1	CXVB_CONER	P58783	conus ermin
305	2	5.9	30	1	CYO1_VIOOD	P82230	viola odora
306	2	5.9	30	1	CYO5_VIOOD	P58437	viola odora
307	2	5.9	30	1	CYO8_VIOOD	P58440	viola odora
308	2	5.9	30	1	DEF2_MACMU	P82317	macaca mula
309	2	5.9	30	1	DIDH_COMTE	P80702	comamonas t
310	2	5.9	30	1	DIU2_HYLLI	P82015	hyles linea
311	2	5.9	30	1	DIU2_MANSE	P24858	manduca sex
312	2	5.9	30	1	END2_ONCKE	P01205	oncorhynchu
313	2	5.9	30	1	FIBR_PANIN	P22775	panulirus i
314	2	5.9	30	1	FMBB_BACNO	P17829	bacteroides
315	2	5.9	30	1	HCY2_HOMAM	P82297	homarus ame
316	2	5.9	30	1	HYP4_HYBPA	P58445	hybanthus p
317	2	5.9	30	1	IHFB_RHILE	P80606	rhizobium l
318	2	5.9	30	1	ITI1_LAGLE	P26771	lagenaria l
319	2	5.9	30	1	ITR1_CITLA	P11969	citrullus l
320	2	5.9	30	1	ITR1_MOMCH	P10294	momordica c
321	2	5.9	30	1	ITR2_ECBEL	P12071	ecballium e
322	2	5.9	30	1	ITR2_LUFCY	P25850	luffa cylin
323	2	5.9	30	1	ITR3_CUCMC	P32041	cucumis mel
324	2	5.9	30	1	ITR3_MOMCO	P82410	momordica c
325	2	5.9	30	1	ITR4_CUCSA	P10292	cucumis sat
326	2	5.9	30	1	ITR6_CYCPE	P83397	cyclanthera
327	2	5.9	30	1	ITR7_CYCPE	P83398	cyclanthera
328	2	5.9	30	1	KAB5_OLDAF	P58456	oldenlandia
329	2	5.9	30	1	LAS1_PIG	P80171	sus scrofa
330	2	5.9	30	1	LEAH_PHAVU	P81870	phaseolus v
331	2	5.9	30	1	MDH_HELGE	P80037	heliobacter
332	2	5.9	30	1	MMAL_DERMI	P16312	dermatophag
333	2	5.9	30	1	NU5M_PISOC	P24999	pisaster oc
334	2	5.9	30	1	NUO2_SOLTU	P80268	solanum tub
335	2	5.9	30	1	P2CO_ARTSP	P37365	arthrobacte
336	2	5.9	30	1	PCCA_MYXXA	P81185	myxococcus
337	2	5.9	30	1	PCG1_PACGO	P82414	pachycondyl
338	2	5.9	30	1	PCG5_PACGO	P82418	pachycondyl
339	2	5.9	30	1	PETN_NEPOL	Q9tl01	nephroselmi
340	2	5.9	30	1	PLF4_RABIT	P83470	oryctolagus
341	2	5.9	30	1	PLMS_SQUAC	P82542	squalus aca
342	2	5.9	30	1	PMGY_CANAL	P82612	candida alb
343	2	5.9	30	1	PRT1_CLUPA	P02335	clupea pall
344	2	5.9	30	1	PRT2_ONCMY	P02331	oncorhynchu
345	2	5.9	30	1	PRT3_ONCMY	P02332	oncorhynchu
346	2	5.9	30	1	PRT4_ONCMY	P02333	oncorhynchu
347	2	5.9	30	1	PRTB_ONCMY	P12819	oncorhynchu
348	2	5.9	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
349	2	5.9	30	1	PSAM_MESVI	Q9mus2	mesostigma
350	2	5.9	30	1	PSAM_ODOSI	P49487	odontella s
351	2	5.9	30	1	PSAM_PINTH	P41601	pinus thunb
352	2	5.9	30	1	PSAM_PORPU	P51395	porphyra pu
353	2	5.9	30	1	PYSD_METBA	P80524	methanosarc
354	2	5.9	30	1	RIPS_MOMCO	P20655	momordica c
355	2	5.9	30	1	RKGG_LEPKE	P21587	lepidochely
356	2	5.9	30	1	RNP_ODOVI	P19640	odocoileus
357	2	5.9	30	1	SCK2_TITSE	P08816	tityus serr
358	2	5.9	30	1	SCX2_CENLI	P18927	centruroides
359	2	5.9	30	1	SILU_RHIPU	P02885	rhizomucor

360	2	5.9	30	1	TAT_HV1ZH	P12512	human immun
361	2	5.9	30	1	TL1X_SPIOL	P82537	spinacia ol
362	2	5.9	30	1	TL29_SPIOL	P81833	spinacia ol
363	2	5.9	30	1	TX2_HETVE	P58426	heteropoda
364	2	5.9	30	1	UC35_MAIZE	P80641	zea mays (m
365	2	5.9	30	1	UDDP_SULAC	P80143	sulfolobus
366	2	5.9	30	1	URE1_ECOLI	Q03284	escherichia
367	2	5.9	30	1	VAA1_EQUAR	Q04236	equisetum a
368	2	5.9	30	1	VAA1_PSINU	Q04237	psilotum nu
369	2	5.9	30	1	VAA2_PSINU	Q04239	psilotum nu
370	2	5.9	30	1	VATN_BOVIN	P81134	bos taurus
371	2	5.9	30	1	VG03_BPPF1	P25137	bacterioph
372	2	5.9	30	1	VPU_HV1SC	P05948	human immun
373	2	5.9	30	1	VTTA_BPT3	P20837	bacterioph
374	2	5.9	30	1	Y161_TREPA	O83196	treponema p
375	2	5.9	30	1	Y357_BORBU	O51332	borrelia bu
376	2	5.9	30	1	Y425_BORBU	O51386	borrelia bu
377	2	5.9	30	1	Y573_TREPA	O83583	treponema p
378	2	5.9	30	1	Y932_TREPA	O83902	treponema p
379	2	5.9	30	1	YCCB_ECOLI	P24244	escherichia
380	2	5.9	31	1	BCAM_PIG	O19098	sus scrofa
381	2	5.9	31	1	CIRB_CHAPA	P56879	chassalia p
382	2	5.9	31	1	COG5_BOVIN	P83437	bos taurus
383	2	5.9	31	1	COX4_NEUCR	P06809	neurospora
384	2	5.9	31	1	CTRP_PENMO	P35002	penaeus mon
385	2	5.9	31	1	CXD6_CONNI	P56710	conus nigro
386	2	5.9	31	1	CXG6_CONTE	P58922	conus texti
387	2	5.9	31	1	DEJP_DROME	P81160	drosophila
388	2	5.9	31	1	EFTU_STRLU	P52390	streptomyce
389	2	5.9	31	1	ENDB_CAMDR	P01203	camelus dro
390	2	5.9	31	1	ER29_BOVIN	P81623	bos taurus
391	2	5.9	31	1	ETFD_PARDE	P55932	paracoccus
392	2	5.9	31	1	FIBB_CANFA	P02677	canis famil
393	2	5.9	31	1	GP37_BPSP1	O48393	bacterioph
394	2	5.9	31	1	GT_SERMA	P22416	serratia ma
395	2	5.9	31	1	HBA_MACEU	P81043	macropus eu
396	2	5.9	31	1	HCY1_HOMAM	P82296	homarus ame
397	2	5.9	31	1	HCY2_MAISQ	P82303	maia squina
398	2	5.9	31	1	HEM2_PHAGO	P27687	phascolopsi
399	2	5.9	31	1	LC70_LACPA	P80959	lactobacill
400	2	5.9	31	1	LPRM_ECOLI	P10739	escherichia
401	2	5.9	31	1	MDH_STRAR	P19982	streptomyce
402	2	5.9	31	1	PETL_ANASP	Q8yvq2	anabaena sp
403	2	5.9	31	1	PETL_ARATH	P56776	arabidopsis
404	2	5.9	31	1	PETL_BETVU	P46612	beta vulgar
405	2	5.9	31	1	PETL_CHLVU	P56306	chlorella v
406	2	5.9	31	1	PETL_GUIITH	O78468	guillardia
407	2	5.9	31	1	PETL_MAIZE	P19445	zea mays (m
408	2	5.9	31	1	PETL_ODOSI	P49524	odontella s
409	2	5.9	31	1	PETL_OENHO	Q9mtk4	oenothera h
410	2	5.9	31	1	PETL_ORYSA	P12180	oryza sativ
411	2	5.9	31	1	PETL_PORPU	P51221	porphyra pu
412	2	5.9	31	1	PETL_PSINU	Q8wi03	psilotum nu
413	2	5.9	31	1	PETL_SPIOL	Q9m310	spinacia ol
414	2	5.9	31	1	PETL_WHEAT	P58247	triticum ae
415	2	5.9	31	1	PETM_CYACA	Q9t1r5	cyanidium c
416	2	5.9	31	1	PETN_CYACA	Q9t1r6	cyanidium c

417	2	5.9	31	1	PRT2_CLUPA	P02336	clupea pall
418	2	5.9	31	1	PSAK_ANAVA	P23317	anabaena va
419	2	5.9	31	1	PSAM_CYAPA	P48185	cyanophora
420	2	5.9	31	1	PSAM_EUGGR	P31479	euglena gra
421	2	5.9	31	1	PSBK_SYNVU	P19054	synechococc
422	2	5.9	31	1	PSBM_MESVI	Q9muq7	mesostigma
423	2	5.9	31	1	PSBT_CHLRE	P37256	chlamydomon
424	2	5.9	31	1	PSBT_CHLVU	P56327	chlorella v
425	2	5.9	31	1	PSBT_CYAPA	P48109	cyanophora
426	2	5.9	31	1	PSBT_EUGGR	P20176	euglena gra
427	2	5.9	31	1	PSBT_MESVI	Q9muv6	mesostigma
428	2	5.9	31	1	PSBT_PORPU	P51323	porphyra pu
429	2	5.9	31	1	PYSG_METBA	P80523	methanosarc
430	2	5.9	31	1	RECX_METCL	P37865	methylomona
431	2	5.9	31	1	RL21_STRTR	P48956	streptococc
432	2	5.9	31	1	SARL_HUMAN	O00631	homo sapien
433	2	5.9	31	1	SC37_MESMA	P83407	mesobuthus
434	2	5.9	31	1	SCK5_ANDMA	P31719	androctonus
435	2	5.9	31	1	SCKL_LEIQH	P16341	leiurus qui
436	2	5.9	31	1	SODC_STRHE	P81163	striga herm
437	2	5.9	31	1	TX3_HETVE	P58427	heteropoda
438	2	5.9	31	1	TXA3_PARAC	P09949	parasicyoni
439	2	5.9	31	1	Y191_BORBU	O51209	borrelia bu
440	2	5.9	31	1	Y3KD_BPCHP	P19187	bacterioph
441	2	5.9	31	1	Y603_ARCFU	O29652	archaeoglob
442	2	5.9	32	1	A2M_PACLE	P20738	pacifastacu
443	2	5.9	32	1	APL3_DIAGR	P81471	diatraea gr
444	2	5.9	32	1	ATP0_PIG	P80021	sus scrofa
445	2	5.9	32	1	ATP7_SPIOL	P80088	spinacia ol
446	2	5.9	32	1	ATPO_SPIOL	P80087	spinacia ol
447	2	5.9	32	1	B4G1_RAT	P80225	r beta-1,4-
448	2	5.9	32	1	CAAP_MICEC	P21162	micromonosp
449	2	5.9	32	1	CAL0_BOVIN	P01260	bos taurus
450	2	5.9	32	1	CAL0_PIG	P01259	sus scrofa
451	2	5.9	32	1	CAR1_ECHCA	Q9prp9	echis carin
452	2	5.9	32	1	CEC_OIKKI	P83420	oiketicus k
453	2	5.9	32	1	COA1_BPIF1	O80295	bacterioph
454	2	5.9	32	1	COA1_BPIKE	P03676	bacterioph
455	2	5.9	32	1	COA2_BPFD	P03677	bacterioph
456	2	5.9	32	1	CRP_PLEPL	P12245	pleuronecte
457	2	5.9	32	1	CXG7_CONPE	P56711	conus penna
458	2	5.9	32	1	CYBL_RHOGR	P32953	rhodotorula
459	2	5.9	32	1	ER29_CHICK	P81628	gallus gall
460	2	5.9	32	1	ER29_TRIVU	P81629	trichosurus
461	2	5.9	32	1	ERH_PIG	P80230	sus scrofa
462	2	5.9	32	1	FER_PORCR	P18821	porphyridiu
463	2	5.9	32	1	FRIH_ANAPL	P80145	anas platyr
464	2	5.9	32	1	GHR4_RAT	P33581	rattus norv
465	2	5.9	32	1	GLB4_LAMSP	P20413	lamellibrac
466	2	5.9	32	1	GT82_DICLA	P82608	dicentrarch
467	2	5.9	32	1	H2AZ_ONCMY	P22647	oncorhynch
468	2	5.9	32	1	HCYC_CHEDE	P83172	cherax dest
469	2	5.9	32	1	IAPP_BOVIN	Q28207	bos taurus
470	2	5.9	32	1	IAPP_PIG	Q29119	sus scrofa
471	2	5.9	32	1	IAPP_SAGOE	Q28934	saguinus oe
472	2	5.9	32	1	IAPP_SHEEP	Q28605	ovis aries
473	2	5.9	32	1	ILVB_ENTAE	Q09129	enterobacte

474	2	5.9	32	1	ITR2_CUCSA	P10291	cucumis sat
475	2	5.9	32	1	LPID_ECOLI	P03060	escherichia
476	2	5.9	32	1	LPID_EDWTA	P08140	edwardsiell
477	2	5.9	32	1	LPIV_ECOLI	P03061	escherichia
478	2	5.9	32	1	MDH_NITAL	P10887	nitzschia a
479	2	5.9	32	1	MIFH_TRITR	P81748	trichuris t
480	2	5.9	32	1	NEUB_PIG	P01297	sus scrofa
481	2	5.9	32	1	OVOS_ANAPL	P20739	anas platyr
482	2	5.9	32	1	P1SM_LOXIN	P83045	loxosceles
483	2	5.9	32	1	PA22_AGKHP	P18997	agkistrodon
484	2	5.9	32	1	PA2_RHONO	P43318	rhophilema n
485	2	5.9	32	1	PETL_CHLRE	P50369	chlamydomon
486	2	5.9	32	1	PETM_PORPU	P51275	porphyra pu
487	2	5.9	32	1	PHNS_DESMU	P13062	desulfovibr
488	2	5.9	32	1	PRI3_ONCMY	P02330	oncorhynchu
489	2	5.9	32	1	PRT1_ONCKE	P02327	oncorhynchu
490	2	5.9	32	1	PRT4_SCYCA	P30259	scyliorhinu
491	2	5.9	32	1	PRT5_ONCMY	P02334	oncorhynchu
492	2	5.9	32	1	PRT6_ONCMY	P08145	oncorhynchu
493	2	5.9	32	1	PRT7_ONCMY	P08146	oncorhynchu
494	2	5.9	32	1	PRT8_ONCMY	P12817	oncorhynchu
495	2	5.9	32	1	PRT9_ONCMY	P08147	oncorhynchu
496	2	5.9	32	1	PRTA_ONCMY	P12818	oncorhynchu
497	2	5.9	32	1	PRTE_HALME	P28308	halobacteri
498	2	5.9	32	1	PRT_ORYLA	Q91185	oryzias lat
499	2	5.9	32	1	PSAM_MARPO	P31590	marchantia
500	2	5.9	32	1	PSBT_CYACA	O19927	cyanidium c
501	2	5.9	32	1	PSBT_GUIITH	O78512	guillardia
502	2	5.9	32	1	PSBZ_EUGAN	Q8s195	euglena ana
503	2	5.9	32	1	PSBZ_EUGGA	Q8s193	euglena gra
504	2	5.9	32	1	PSBZ_EUGMY	Q8s191	euglena myx
505	2	5.9	32	1	RIP2_PHYDI	P34967	phytolacca
506	2	5.9	32	1	RK1_RABIT	P81655	oryctolagus
507	2	5.9	32	1	RS19_YEREN	Q56847	yersinia en
508	2	5.9	32	1	SCK2_CENNO	P58504	centruroide
509	2	5.9	32	1	TAT_SIVM2	P05912	simian immu
510	2	5.9	32	1	TRYP_PENMO	P35050	penaeus mon
511	2	5.9	32	1	TX29_PHONI	P29426	phoneutria
512	2	5.9	32	1	TXP7_APTSC	P49271	aptostichus
513	2	5.9	32	1	UC09_MAIZE	P80615	zea mays (m
514	2	5.9	32	1	Y169_TREPA	O83199	treponema p
515	2	5.9	32	1	Y433_BORBU	O51394	borrelia bu
516	2	5.9	32	1	YH17_HAEIN	P44295	haemophilus
517	2	5.9	32	1	YSCA_YEREN	Q01242	yersinia en
518	2	5.9	32	1	YTK3_ILTVT	P23985	infectious
519	2	5.9	33	1	ACT_DICVI	Q24733	dictyocaulu
520	2	5.9	33	1	ANP3_MYOSC	P04367	myoxocephal
521	2	5.9	33	1	ANP5_MYOAE	P20421	myoxocephal
522	2	5.9	33	1	ATP7_SOLTU	P80496	solanum tub
523	2	5.9	33	1	BR2A_RANES	P40837	rana escule
524	2	5.9	33	1	BR2B_RANES	P40838	rana escule
525	2	5.9	33	1	BR2E_RANES	P32413	rana escule
526	2	5.9	33	1	BR2_RANBP	P32424	rana brevip
527	2	5.9	33	1	CECB_HELVI	P83414	heliothis v
528	2	5.9	33	1	CECC_HELVI	P83415	heliothis v
529	2	5.9	33	1	COA1_BPF	P03675	bacterioph
530	2	5.9	33	1	COA2_BPI22	P15414	bacterioph

531	2	5.9	33	1	COXL_ONCMY	P80330	oncorhynchu
532	2	5.9	33	1	CU89_HUMAN	P59042	homo sapien
533	2	5.9	33	1	CXBW_CONRA	P58804	conus radia
534	2	5.9	33	1	CXO_CONVE	P83301	conus ventr
535	2	5.9	33	1	DBB2_DOLAU	P83376	dolabella a
536	2	5.9	33	1	DEF1_MESAU	P81465	mesocricetu
537	2	5.9	33	1	DEF3_MESAU	P81467	mesocricetu
538	2	5.9	33	1	DHE3_PIG	P42174	sus scrofa
539	2	5.9	33	1	FER_PORAE	P18820	porphyridiu
540	2	5.9	33	1	GAST_CAVPO	P06885	cavia porce
541	2	5.9	33	1	GAST_CHIBR	P10034	chinchilla
542	2	5.9	33	1	GAST_DIDMA	P33713	didelphis m
543	2	5.9	33	1	GGN1_RANRU	P80395	rana rugosa
544	2	5.9	33	1	GGN2_RANRU	P80396	rana rugosa
545	2	5.9	33	1	GGN3_RANRU	P80397	rana rugosa
546	2	5.9	33	1	HF40_MAIZE	P82865	zea mays (m
547	2	5.9	33	1	HOXU_RHOOP	P22659	rhodococcus
548	2	5.9	33	1	LPPY_SALTY	P08522	salmonella
549	2	5.9	33	1	LPRH_ECOLI	P37324	escherichia
550	2	5.9	33	1	LYC2_HORSE	P81710	equus cabal
551	2	5.9	33	1	MBP1_MAIZE	P28794	zea mays (m
552	2	5.9	33	1	MHAA_STRCH	P80435	streptomyce
553	2	5.9	33	1	MYMY_MYTED	P81614	mytilus edu
554	2	5.9	33	1	OTCC_PSEPU	P11727	pseudomonas
555	2	5.9	33	1	PBAN_LYMDI	P43511	lymantria d
556	2	5.9	33	1	PEN3_ADECU	P35987	canine aden
557	2	5.9	33	1	PETM_CYAPA	P48366	cyanophora
558	2	5.9	33	1	PETM_SYNEL	Q8dj15	synechococc
559	2	5.9	33	1	PK1_DICDI	P34101	dictyosteli
560	2	5.9	33	1	PK5_DICDI	P34104	dictyosteli
561	2	5.9	33	1	PRI1_ONCMY	P02326	oncorhynchu
562	2	5.9	33	1	PRI2_ONCMY	P02328	oncorhynchu
563	2	5.9	33	1	PRTB_MUGCE	P08130	mugil cepha
564	2	5.9	33	1	PRTL_ECOLI	P02338	escherichia
565	2	5.9	33	1	PSAI_SPIOL	P17228	spinacia ol
566	2	5.9	33	1	PSAK_CUCSA	P42051	cucumis sat
567	2	5.9	33	1	PSBT_ARATH	P37259	arabidopsis
568	2	5.9	33	1	PSBT_MAIZE	P37257	zea mays (m
569	2	5.9	33	1	RL21_XENLA	P49628	xenopus lae
570	2	5.9	33	1	RL26_XENLA	P49629	xenopus lae
571	2	5.9	33	1	RL28_XENLA	P46780	xenopus lae
572	2	5.9	33	1	RL4_HALCU	P05967	halobacteri
573	2	5.9	33	1	RPOC_HETCA	P36441	heterosigma
574	2	5.9	33	1	RRPO_BPBZ1	P09674	bacterioph
575	2	5.9	33	1	RS4_XENLA	P49401	xenopus lae
576	2	5.9	33	1	RT25_BOVIN	P82669	bos taurus
577	2	5.9	33	1	RUGA_RANRU	P80954	rana rugosa
578	2	5.9	33	1	RUGB_RANRU	P80955	rana rugosa
579	2	5.9	33	1	SCX9_BUTOC	P04099	buthus occi
580	2	5.9	33	1	THIO_CLOST	P81109	clostridium
581	2	5.9	33	1	TX1_HETVE	P58425	heteropoda
582	2	5.9	33	1	TXH1_SELHU	P56676	selenocosmi
583	2	5.9	33	1	TXN3_SELHA	P83464	selenocosmi
584	2	5.9	33	1	VT1B_RAT	P58200	rattus norv
585	2	5.9	33	1	Y474_BORBU	O51430	borrelia bu
586	2	5.9	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
587	2	5.9	33	1	Y656_TREPA	O83662	treponema p

588	2	5.9	33	1	Y849_BORBU	051789	borrelia bu
589	2	5.9	33	1	YC12_CHLRE	P50370	chlamydomon
590	2	5.9	33	1	YC12_MARPO	P31560	marchantia
591	2	5.9	33	1	YC12_MESVI	Q9mus3	mesostigma
592	2	5.9	33	1	YC12_NEPOL	Q9tky6	nephroselmi
593	2	5.9	33	1	YC12_PINTH	P41600	pinus thunb
594	2	5.9	33	1	YL74_ARCFU	O28108	archaeoglob
595	2	5.9	33	1	YLCH_BP82	Q37869	bacteriopha
596	2	5.9	33	1	YLCH_ECOLI	Q47268	escherichia
597	2	5.9	34	1	AMP2_CHICK	P80390	gallus gall
598	2	5.9	34	1	ASPG_PIG	P30918	sus scrofa
599	2	5.9	34	1	BR2C_RANES	P40839	rana escule
600	2	5.9	34	1	COL_CHICK	P11148	gallus gall
601	2	5.9	34	1	COXA_THETH	P82543	thermus the
602	2	5.9	34	1	COXG_THUOB	P80976	thunnus obe
603	2	5.9	34	1	CXGS_CONGE	P15472	conus geogr
604	2	5.9	34	1	DEF2_RABIT	P07468	oryctolagus
605	2	5.9	34	1	DEF7_RABIT	P80223	oryctolagus
606	2	5.9	34	1	ECAB_ECTTU	P49344	ectatomma t
607	2	5.9	34	1	EF2_RABIT	P55823	oryctolagus
608	2	5.9	34	1	EGGR_APLCA	P01363	aplysia cal
609	2	5.9	34	1	H1S_STRPU	P19376	strongyloce
610	2	5.9	34	1	HS7S_CUCMA	P31082	cucurbita m
611	2	5.9	34	1	ITR1_MOMCO	P82408	momordica c
612	2	5.9	34	1	ITR2_MOMCO	P82409	momordica c
613	2	5.9	34	1	LPTN_PROVU	P28779	proteus vul
614	2	5.9	34	1	M44E_HUMAN	Q96pgl	homo sapien
615	2	5.9	34	1	MYTA_MYTED	P81612	mytilus edu
616	2	5.9	34	1	MYTB_MYTED	P81613	mytilus edu
617	2	5.9	34	1	PETM_ANASP	Q9f4w2	anabaena sp
618	2	5.9	34	1	PRT1_SAROR	P25327	sarda orien
619	2	5.9	34	1	PRT1_SCOSC	P83264	scomber sco
620	2	5.9	34	1	PRT1_THUTH	P02321	thunnus thy
621	2	5.9	34	1	PRT2_SCOSC	P83265	scomber sco
622	2	5.9	34	1	PRT2_THUTH	P02322	thunnus thy
623	2	5.9	34	1	PRT_DICLA	Q9ps27	dicentrarch
624	2	5.9	34	1	PRT_PERFV	P29629	perca flave
625	2	5.9	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
626	2	5.9	34	1	PSAI_OENHO	Q9mtl2	oenothera h
627	2	5.9	34	1	PSAI_SOYBN	P49159	glycine max
628	2	5.9	34	1	PSBM_ARATH	P12169	arabidopsis
629	2	5.9	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
630	2	5.9	34	1	PSBM_CHLRE	P92277	chlamydomon
631	2	5.9	34	1	PSBM_MAIZE	P48189	zea mays (m
632	2	5.9	34	1	PSBM_MARPO	P12168	marchantia
633	2	5.9	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
634	2	5.9	34	1	PSBM_OENHO	Q9mtm8	oenothera h
635	2	5.9	34	1	PSBM_PEA	P34833	pisum sativ
636	2	5.9	34	1	PSBM_PSINU	Q8wi22	psilotum nu
637	2	5.9	34	1	PSBM_WHEAT	Q9xps6	triticum ae
638	2	5.9	34	1	PSBT_TOBAC	P12184	nicotiana t
639	2	5.9	34	1	PSPC_BOVIN	P15783	bos taurus
640	2	5.9	34	1	PSPC_CANFA	P22397	canis famil
641	2	5.9	34	1	PTU1_PEITU	P58606	peirates tu
642	2	5.9	34	1	PYSB_METBA	P80522	methanosarc
643	2	5.9	34	1	RNL1_PIG	P15466	sus scrofa
644	2	5.9	34	1	RR2_OCHNE	Q40606	ochrosphaer

645	2	5.9	34	1	SCXM_SCOMA	P80719	scorpio mau
646	2	5.9	34	1	SMS_MYXGL	P19209	myxine glut
647	2	5.9	34	1	THEM_MALSU	P13858	malbranchea
648	2	5.9	34	1	TX33_PHONI	P81789	phoneutria
649	2	5.9	34	1	TXP5_BRASM	P49266	brachypelma
650	2	5.9	34	1	VLYS_BPM1	P08229	bacteriopha
651	2	5.9	34	1	VPU_HV1W2	P08808	human immun
652	2	5.9	34	1	Y05J_BPT4	P39239	bacteriopha
653	2	5.9	34	1	Y224_TREPA	O83253	treponema p
654	2	5.9	34	1	Y848_BORBU	O51788	borrelia bu
655	2	5.9	34	1	Y870_HAEIN	P44065	haemophilus
656	2	5.9	34	1	Y967_HAEIN	P44086	haemophilus
657	2	5.9	34	1	YC12_GUITH	O78460	guillardia
658	2	5.9	34	1	YC12_ODOSI	P49529	odontella s
659	2	5.9	34	1	YC12_PORPU	P51385	porphyra pu
660	2	5.9	34	1	YC12_SKECO	O96797	skeletonema
661	2	5.9	34	1	YMIA_AGRTU	P38437	agrobacteri
662	2	5.9	34	1	Z33B_HUMAN	Q06731	homo sapien
663	2	5.9	35	1	ADO1_AGRDO	P58608	agriosphodr
664	2	5.9	35	1	C550_BACHA	P80091	bacillus ha
665	2	5.9	35	1	CEC4_BOMMO	P14666	bombyx mori
666	2	5.9	35	1	CECA_HELVI	P83413	heliothis v
667	2	5.9	35	1	CECB_ANTPE	P01509	antheraea p
668	2	5.9	35	1	CHI1_CASSA	P29137	castanea sa
669	2	5.9	35	1	D3HI_RABIT	P32185	oryctolagus
670	2	5.9	35	1	DEFB_MYTED	P81611	mytilus edu
671	2	5.9	35	1	END4_YEREN	P42691	yersinia en
672	2	5.9	35	1	ERFK_KLEAE	Q08599	klebsiella
673	2	5.9	35	1	EXE2_HEL SU	P04204	heloderma s
674	2	5.9	35	1	FAS_CAPHI	P08757	capra hircu
675	2	5.9	35	1	FLAV_NOSSM	P35707	nostoc sp.
676	2	5.9	35	1	GBGU_MOUSE	Q61017	mus musculu
677	2	5.9	35	1	GRDB_CLOPU	P55793	clostridium
678	2	5.9	35	1	GUR_GYMSY	P25810	gymnema syl
679	2	5.9	35	1	HMWC_DESGI	P38588	desulfovibr
680	2	5.9	35	1	IAAC_HORVU	P34951	hordeum vul
681	2	5.9	35	1	KPPR_PINPS	P81664	pinus pinas
682	2	5.9	35	1	LCGB_LACLA	P36962	lactococcus
683	2	5.9	35	1	NEF_HV1H3	P05854	human immun
684	2	5.9	35	1	PBP1_LYMDI	P34176	lymantria d
685	2	5.9	35	1	PBP2_LYMDI	P34177	lymantria d
686	2	5.9	35	1	PBP_HYACE	P34175	hyalophora
687	2	5.9	35	1	PHI1_MYTCA	P35422	mytilus cal
688	2	5.9	35	1	PSAI_CYAPA	P48116	cyanophora
689	2	5.9	35	1	PSBM_SYNY3	P72701	synechocyst
690	2	5.9	35	1	PSBT_OENHO	P37258	oenothera h
691	2	5.9	35	1	PSBT_ORYSA	P12183	oryza sativ
692	2	5.9	35	1	PSBT_PINTH	P41625	pinus thunb
693	2	5.9	35	1	PSPC_PIG	P15785	sus scrofa
694	2	5.9	35	1	RL32_HALCU	P05965	halobacteri
695	2	5.9	35	1	SCKB_PANIM	P55928	pandinus im
696	2	5.9	35	1	SCKG_PANIM	Q10726	pandinus im
697	2	5.9	35	1	SCX5_BUTEU	P15222	buthus eupe
698	2	5.9	35	1	SCXP_ANDMA	P01498	androctonus
699	2	5.9	35	1	SMS_LAMFL	Q9prro	lampetra fl
700	2	5.9	35	1	SPRC_PIG	P20112	sus scrofa
701	2	5.9	35	1	THPA_THADA	P21381	thaumatococ

702	2	5.9	35	1	TXAG_AGEOP	P31328	agelena opu
703	2	5.9	35	1	TXH4_SELHU	P83303	selenocosmi
704	2	5.9	35	1	TXKS_STOHE	P29187	stoichactis
705	2	5.9	35	1	TXN4_SELHA	P83471	selenocosmi
706	2	5.9	35	1	VL3_PAPVD	P06919	deer papill
707	2	5.9	35	1	VSPA_CERVI	P18692	cerastes vi
708	2	5.9	35	1	WSP7_PINPS	P81086	pinus pinas
709	2	5.9	35	1	Y320_BORBU	O51299	borrelia bu
710	2	5.9	35	1	Y37_BPT3	P20325	bacteriopha
711	2	5.9	35	1	Y644_ARCFU	O29613	archaeoglob
712	2	5.9	35	1	Y845_BORBU	O51785	borrelia bu
713	2	5.9	35	1	Y847_BORBU	O51787	borrelia bu
714	2	5.9	35	1	YC12_CYACA	Q9tlx0	cyanidium c
715	2	5.9	35	1	YC69_ARCFU	O28999	archaeoglob
716	2	5.9	35	1	YQB5_CAEEL	Q09258	caenorhabdi
717	2	5.9	36	1	AMPL_PIG	P28839	sus scrofa
718	2	5.9	36	1	ANFV_ANGJA	P22642	anguilla ja
719	2	5.9	36	1	C3L1_BOVIN	P30922	bos taurus
720	2	5.9	36	1	CBBA_NITVU	P37102	nitrobacter
721	2	5.9	36	1	CECD_ANTPE	P01511	antheraea p
722	2	5.9	36	1	CYC7_GEOME	P81894	geobacter m
723	2	5.9	36	1	DESR_DESGI	P00273	desulfovibr
724	2	5.9	36	1	F4RE_METOG	P80951	methanogeni
725	2	5.9	36	1	GLU1_ORENI	P81026	oreochromis
726	2	5.9	36	1	GLUC_HYDCO	P09682	hydrolagus
727	2	5.9	36	1	H1L5_ENSMI	P27203	ensis minor
728	2	5.9	36	1	HBB_PONPY	Q9tt34	pongo pygma
729	2	5.9	36	1	IAA_STRAU	P04082	streptomyce
730	2	5.9	36	1	IOB1_ISYOB	P58609	isyndus obs
731	2	5.9	36	1	KAD_STRGR	P53398	streptomyce
732	2	5.9	36	1	LHG_RHOVI	P04126	rhodopseudo
733	2	5.9	36	1	LYOX_PIG	P45845	sus scrofa
734	2	5.9	36	1	MFA1_YEAST	P34165	saccharomyc
735	2	5.9	36	1	MPG2_DACGL	Q41183	dactylis gl
736	2	5.9	36	1	MYPC_RAT	P56741	rattus norv
737	2	5.9	36	1	NEUH_CARCA	P11975	cardisoma c
738	2	5.9	36	1	NEUY_GADMO	P80167	gadus morhu
739	2	5.9	36	1	NEUY_ONCMY	P29071	oncorhynchu
740	2	5.9	36	1	NEUY_RABIT	P09640	oryctolagus
741	2	5.9	36	1	NEUY_RANRI	P29949	rana ridibu
742	2	5.9	36	1	NIFH_ENTAG	P26249	enterobacte
743	2	5.9	36	1	NLTP_PINPI	P26912	pinus pinea
744	2	5.9	36	1	NUCM_SOLTU	P80264	solanum tub
745	2	5.9	36	1	OST2_CHICK	P80897	gallus gall
746	2	5.9	36	1	PAHO_ALLMI	P06305	alligator m
747	2	5.9	36	1	PAHO_ANSAN	P06304	anser anser
748	2	5.9	36	1	PAHO_CERSI	P37999	ceratotheri
749	2	5.9	36	1	PAHO_DIDMA	P18107	didelphis m
750	2	5.9	36	1	PAHO_EQUZE	P38000	equus zebra
751	2	5.9	36	1	PAHO_ERIEU	P41335	erinaceus e
752	2	5.9	36	1	PAHO_LARAR	P41337	larus argen
753	2	5.9	36	1	PAHO_MACMU	P33684	macaca mula
754	2	5.9	36	1	PAHO_RABIT	P41336	oryctolagus
755	2	5.9	36	1	PAHO_RANCA	P15427	rana catesb
756	2	5.9	36	1	PAHO_RANTE	P31229	rana tempor
757	2	5.9	36	1	PAHO_STRCA	P11967	struthio ca
758	2	5.9	36	1	PAHO_TAPPI	P39659	tapirus pin

759	2	5.9	36	1	PGKH_CHLFU	P36232	chlorella f
760	2	5.9	36	1	PSAD_PEA	P20117	pisum sativ
761	2	5.9	36	1	PSAH_PEA	P20121	pisum sativ
762	2	5.9	36	1	PSAI_ANGLY	P28251	angiopteris
763	2	5.9	36	1	PSAI_BRAOL	Q31909	brassica ol
764	2	5.9	36	1	PSAI_CARCL	Q9gdv2	carpobrotus
765	2	5.9	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
766	2	5.9	36	1	PSAI_CHLVU	P58214	chlorella v
767	2	5.9	36	1	PSAI_CYACA	Q9tm24	cyanidium c
768	2	5.9	36	1	PSAI_GUITH	O78462	guillardia
769	2	5.9	36	1	PSAI_HORVU	P13165	hordeum vul
770	2	5.9	36	1	PSAI_MAIZE	P30980	zea mays (m
771	2	5.9	36	1	PSAI_MARPO	P12185	marchantia
772	2	5.9	36	1	PSAI_MESVI	Q9muq4	mesostigma
773	2	5.9	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
774	2	5.9	36	1	PSAI_ORYSA	P12186	oryza sativ
775	2	5.9	36	1	PSAI_PICAB	O47040	picea abies
776	2	5.9	36	1	PSAI_PORPU	P51387	porphyra pu
777	2	5.9	36	1	PSAI_PSINU	Q8wi10	psilotum nu
778	2	5.9	36	1	PSAI_SKECO	O96813	skeletonema
779	2	5.9	36	1	PSAI_TOBAC	P12187	nicotiana t
780	2	5.9	36	1	PSAI_WHEAT	P25410	triticum ae
781	2	5.9	36	1	PSBI_ARATH	P09970	arabidopsis
782	2	5.9	36	1	PSBI_HORVU	P25876	hordeum vul
783	2	5.9	36	1	PSBI_MARPO	P09969	marchantia
784	2	5.9	36	1	PSBI_ORYSA	P12161	oryza sativ
785	2	5.9	36	1	PSBI_PINTH	P41599	pinus thunb
786	2	5.9	36	1	PSBI_PSEMZ	P29796	pseudotsuga
787	2	5.9	36	1	PSBM_CHLVU	P56325	chlorella v
788	2	5.9	36	1	PSBM_SYNEL	Q8dha7	synechococc
789	2	5.9	36	1	PSBY_ODOSI	P49543	odontella s
790	2	5.9	36	1	PSBY_PORPU	P51206	porphyra pu
791	2	5.9	36	1	PYY_AMICA	P29205	amia calva
792	2	5.9	36	1	PYY_LEPSP	P09473	lepisosteus
793	2	5.9	36	1	PYY_ONCKI	P09474	oncorhynchu
794	2	5.9	36	1	PYY_PIG	P01305	sus scrofa
795	2	5.9	36	1	PYY_RAJRH	P29206	raja rhina
796	2	5.9	36	1	PYY_RANRI	P29204	rana ridibu
797	2	5.9	36	1	SCK2_CENLL	P45630	centruroide
798	2	5.9	36	1	SCK3_LEIQH	P45660	leiurus qui
799	2	5.9	36	1	SCX1_BUTEU	P15220	buthus eupe
800	2	5.9	36	1	SCXL_LEIQU	P45639	leiurus qui
801	2	5.9	36	1	SPYY_PHYBI	P80952	phyllomedus
802	2	5.9	36	1	TAEK_ACTEQ	P81897	actinia equ
803	2	5.9	36	1	TERN_PSEUS	P82321	pseudacanth
804	2	5.9	36	1	TLN1_CHICK	P54939	gallus gall
805	2	5.9	36	1	TX1B_AGEAP	P15970	agelenopsis
806	2	5.9	36	1	TX35_PHONI	P81791	phoneutria
807	2	5.9	36	1	TXAM_METSE	P11495	metridium s
808	2	5.9	36	1	TXD3_PARLU	P83258	paracoelote
809	2	5.9	36	1	TXJA_HADVE	P82227	hadronyche
810	2	5.9	36	1	TXJB_HADVE	P82226	hadronyche
811	2	5.9	36	1	Y16L_BPT4	P39244	bacteriopha
812	2	5.9	36	1	Y297_ARCFU	O29945	archaeoglob
813	2	5.9	36	1	Y4KD_BPCHP	P19188	bacteriopha
814	2	5.9	36	1	Y609_BORBU	O51554	borrelia bu
815	2	5.9	36	1	Y619_ARCFU	O29636	archaeoglob

816	2	5.9	36	1	Y699_TREPA	083697	treponema p
817	2	5.9	36	1	YC12_CYAPA	P48256	cyanophora
818	2	5.9	36	1	YG50_HAEIN	P44281	haemophilus
819	2	5.9	36	1	YRKG_BACSU	P54434	bacillus su
820	2	5.9	37	1	24KD_PLACH	P14592	plasmodium
821	2	5.9	37	1	AFP4_MALPA	P83138	malva parvi
822	2	5.9	37	1	ANP3_PSEAM	P02733	pseudopleur
823	2	5.9	37	1	ATPO_SOLTU	P80504	solanum tub
824	2	5.9	37	1	B2MG_ORENI	Q03423	oreochromis
825	2	5.9	37	1	CAL1_PIG	P30880	sus scrofa
826	2	5.9	37	1	CAL1_SHEEP	P30881	ovis aries
827	2	5.9	37	1	CALR_RANRI	P31888	rana ridibu
828	2	5.9	37	1	CEC2_MANSE	P14662	manduca sex
829	2	5.9	37	1	CEC3_MANSE	P14663	manduca sex
830	2	5.9	37	1	CEC4_MANSE	P14664	manduca sex
831	2	5.9	37	1	CG2S_LUPAN	P09930	lupinus ang
832	2	5.9	37	1	CHCD_ANTPO	P08931	antheraea p
833	2	5.9	37	1	CS40_STAAU	P81684	staphylococ
834	2	5.9	37	1	CUP4_SARBU	P14486	sarcophaga
835	2	5.9	37	1	DEFA_MYTED	P81610	mytilus edu
836	2	5.9	37	1	ECAA_ECTTU	P49343	ectatomma t
837	2	5.9	37	1	ES2A_RANES	P40845	rana escule
838	2	5.9	37	1	ES2B_RANES	P40846	rana escule
839	2	5.9	37	1	F13A_BOVIN	P12260	bos taurus
840	2	5.9	37	1	GHR3_RAT	P33580	rattus norv
841	2	5.9	37	1	HCYB_CANPG	P83175	cancer pagu
842	2	5.9	37	1	H0XF_RHOOP	P22658	rhodococcus
843	2	5.9	37	1	IAPP_CRIGR	P19890	cricketulus
844	2	5.9	37	1	LPPY_SERMA	P19937	serratia ma
845	2	5.9	37	1	MAUR_PARVE	Q56462	paracoccus
846	2	5.9	37	1	ME20_EUPRA	P26888	euplotes ra
847	2	5.9	37	1	ME22_EUPRA	P58548	euplotes ra
848	2	5.9	37	1	MIBP_PSESP	P04576	pseudomonas
849	2	5.9	37	1	NLT3_VITSX	P80273	vitis sp. (
850	2	5.9	37	1	NLT4_VITSX	P80274	vitis sp. (
851	2	5.9	37	1	NUFM_SOLTU	P80266	solanum tub
852	2	5.9	37	1	OGT1_RABIT	P81436	oryctolagus
853	2	5.9	37	1	OP2A_OXYKI	P83248	oxyopes kit
854	2	5.9	37	1	OP2B_OXYKI	P83249	oxyopes kit
855	2	5.9	37	1	OP2C_OXYKI	P83250	oxyopes kit
856	2	5.9	37	1	OP2D_OXYKI	P83251	oxyopes kit
857	2	5.9	37	1	PETG_ANASP	P58246	anabaena sp
858	2	5.9	37	1	PETG_ANAVA	Q913p7	anabaena va
859	2	5.9	37	1	PETG_ARATH	P56775	arabidopsis
860	2	5.9	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
861	2	5.9	37	1	PETG_CHLEU	P46304	chlamydomon
862	2	5.9	37	1	PETG_CHLRE	Q08362	chlamydomon
863	2	5.9	37	1	PETG_CHLVU	P56305	chlorella v
864	2	5.9	37	1	PETG_CUSRE	P30398	cuscuta ref
865	2	5.9	37	1	PETG_CYAPA	P14236	cyanophora
866	2	5.9	37	1	PETG_EUGGR	P30396	euglena gra
867	2	5.9	37	1	PETG_GUIITH	O78505	guillardia
868	2	5.9	37	1	PETG_MARPO	P12120	marchantia
869	2	5.9	37	1	PETG_MESVI	Q9mun3	mesostigma
870	2	5.9	37	1	PETG_NEPOL	Q9tky8	nephroselmi
871	2	5.9	37	1	PETG_ODOSI	P49470	odontella s
872	2	5.9	37	1	PETG_ORYSA	P12121	oryza sativ

873	2	5.9	37	1	PETG_PINTH	P41614	pinus thunb
874	2	5.9	37	1	PETG_PORPU	P51318	porphyra pu
875	2	5.9	37	1	PETG_PSINU	Q8wi02	psilotum nu
876	2	5.9	37	1	PETG_SKECO	O96811	skeletonema
877	2	5.9	37	1	PETG_SYNEL	Q8dki2	synechococc
878	2	5.9	37	1	PETG_SYNP7	Q9z3g1	synechococc
879	2	5.9	37	1	PIIL_ACHLY	P81720	achromobact
880	2	5.9	37	1	POLN_WEEV	P13896	western equ
881	2	5.9	37	1	PRF1_RAT	P18889	rattus norv
882	2	5.9	37	1	PSAI_ARATH	P56768	arabidopsis
883	2	5.9	37	1	PSAJ_EUGGR	P30394	euglena gra
884	2	5.9	37	1	PSBL_ARATH	P29301	arabidopsis
885	2	5.9	37	1	PSBL_ORYSA	P12166	oryza sativ
886	2	5.9	37	1	PSBM_PINTH	P41608	pinus thunb
887	2	5.9	37	1	PSBY_CYACA	O19893	cyanidium c
888	2	5.9	37	1	PSBY_GUITH	O78433	guillardia
889	2	5.9	37	1	PYY_CHICK	P29203	gallus gall
890	2	5.9	37	1	REV_SIVM2	P08809	simian immu
891	2	5.9	37	1	RK36_ARATH	P12144	arabidopsis
892	2	5.9	37	1	RK36_ASTLO	P24355	astasia lon
893	2	5.9	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
894	2	5.9	37	1	RK36_CHLVU	P56360	chlorella v
895	2	5.9	37	1	RK36_CYACA	Q9tlu9	cyanidium c
896	2	5.9	37	1	RK36_CYAPA	P48131	cyanophora
897	2	5.9	37	1	RK36_EPIVI	P30069	epifagus vi
898	2	5.9	37	1	RK36_EUGGR	P21532	euglena gra
899	2	5.9	37	1	RK36_LOTJA	Q9bbq2	lotus japon
900	2	5.9	37	1	RK36_MARPO	P12142	marchantia
901	2	5.9	37	1	RK36_NEPOL	Q9tl26	nephroselmi
902	2	5.9	37	1	RK36_OENHO	Q9mtj1	oenothera h
903	2	5.9	37	1	RK36_ORYSA	P12143	oryza sativ
904	2	5.9	37	1	RK36_PEA	P07815	pisum sativ
905	2	5.9	37	1	RK36_PINTH	P41631	pinus thunb
906	2	5.9	37	1	RK36_PORPU	P51296	porphyra pu
907	2	5.9	37	1	RK36_PSINU	Q8why9	psilotum nu
908	2	5.9	37	1	RK36_SPIOL	P12230	spinacia ol
909	2	5.9	37	1	RL36_ANASP	Q8ypk0	anabaena sp
910	2	5.9	37	1	RL36_AQUAE	O66487	aquifex aeo
911	2	5.9	37	1	RL36_BACHD	O50631	bacillus ha
912	2	5.9	37	1	RL36_BACST	P07841	bacillus st
913	2	5.9	37	1	RL36_BORBU	O51452	borrelia bu
914	2	5.9	37	1	RL36_CAMJE	Q9pm84	campylobact
915	2	5.9	37	1	RL36_CLOPE	Q8xhu7	clostridium
916	2	5.9	37	1	RL36_DEIRA	Q9rsk0	deinococcus
917	2	5.9	37	1	RL36_HAEIN	P46361	haemophilus
918	2	5.9	37	1	RL36_HELPJ	Q9zjt1	helicobacte
919	2	5.9	37	1	RL36_HELPY	P56058	helicobacte
920	2	5.9	37	1	RL36_LEPIN	Q9xd13	leptospira
921	2	5.9	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
922	2	5.9	37	1	RL36_MYCGE	P47420	mycoplasma
923	2	5.9	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
924	2	5.9	37	1	RL36_MYCPN	P52864	mycoplasma
925	2	5.9	37	1	RL36_MYCPU	Q98q05	mycoplasma
926	2	5.9	37	1	RL36_MYCSP	P38015	mycoplasma
927	2	5.9	37	1	RL36_MYCTU	P45810	mycobacteri
928	2	5.9	37	1	RL36_NEIMA	Q9jrb2	neisseria m
929	2	5.9	37	1	RL36_STRCO	O86772	streptomyce

930	2	5.9	37	1	RL36_SYNPG	O24707	synechococc
931	2	5.9	37	1	RL36_THETH	P80256	thermus the
932	2	5.9	37	1	RL36_THETN	Q8r7x8	thermoanaer
933	2	5.9	37	1	RL36_TREPA	O83239	treponema p
934	2	5.9	37	1	RL36_UREPA	Q9pqn7	ureaplasma
935	2	5.9	37	1	RL36_VIBCH	P78001	vibrio chol
936	2	5.9	37	1	RL7_CLOPA	P05393	clostridium
937	2	5.9	37	1	RS15_HELLE	P52820	helix lucor
938	2	5.9	37	1	RUGC_RANRU	P80956	rana rugosa
939	2	5.9	37	1	SCIT_MESTA	P81761	mesobuthus
940	2	5.9	37	1	SCK2_LEIQH	P45628	leiurus qui
941	2	5.9	37	1	SCK3_BUTOC	P59290	buthus occi
942	2	5.9	37	1	SCK3_PARTR	P83112	parabuthus
943	2	5.9	37	1	SCKA_TITSE	P46114	tityus serr
944	2	5.9	37	1	SCKC_LEIQH	P13487	leiurus qui
945	2	5.9	37	1	SMS_PETMA	P21779	petromyzon
946	2	5.9	37	1	TCTP_TRYBB	P35758	trypanosoma
947	2	5.9	37	1	THHS_HORVU	P33045	hordeum vul
948	2	5.9	37	1	TX21_SELHU	P82959	selenocosmi
949	2	5.9	37	1	TX22_SELHU	P82960	selenocosmi
950	2	5.9	37	1	TXD1_PARLU	P83256	paracoelote
951	2	5.9	37	1	TXD2_PARLU	P83257	paracoelote
952	2	5.9	37	1	TXD4_PARLU	P83259	paracoelote
953	2	5.9	37	1	TXJC_HADVE	P82228	hadronyche
954	2	5.9	37	1	TXM2_AGEAP	P11058	agelenopsis
955	2	5.9	37	1	TXM5_AGEAP	P11061	agelenopsis
956	2	5.9	37	1	TXOF_HADVE	P81599	hadronyche
957	2	5.9	37	1	TXP3_APTSC	P49268	aptostichus
958	2	5.9	37	1	VA1_BPBF2	P19347	bacterioph
959	2	5.9	37	1	VG40_BPML5	Q05250	mycobacteri
960	2	5.9	37	1	VG65_BPPH2	P16515	bacterioph
961	2	5.9	37	1	VG65_BPPZA	P08384	bacterioph
962	2	5.9	37	1	VP64_NPVBM	P41722	bombyx mori
963	2	5.9	37	1	VPU_HV1Z8	P08807	human immun
964	2	5.9	37	1	Y268_ARCFU	O29971	archaeoglob
965	2	5.9	37	1	Y63_BPT7	P03799	bacterioph
966	2	5.9	37	1	Y692_BORBU	O51635	borrelia bu
967	2	5.9	37	1	Y700_BORBU	O51643	borrelia bu
968	2	5.9	37	1	Y762_BORBU	O51703	borrelia bu
969	2	5.9	37	1	Y846_BORBU	O51786	borrelia bu
970	2	5.9	37	1	YBGT_ECOLI	P56100	escherichia
971	2	5.9	37	1	YC12_CHLVU	P56328	chlorella v
972	2	5.9	37	1	YDA3_SCHPO	Q10345	schizosacch
973	2	5.9	37	1	YIM4_BPPH1	P10428	bacterioph
974	2	5.9	37	1	YQGE_BACCA	P28753	bacillus ca
975	2	5.9	37	1	YRYL_CAEL	Q19177	caenorhabdi
976	2	5.9	38	1	A2M_HOMAM	P20737	homarus ame
977	2	5.9	38	1	AFP5_MALPA	P83139	malva parvi
978	2	5.9	38	1	BD01_BOVIN	P46159	bos taurus
979	2	5.9	38	1	BD08_BOVIN	P46166	bos taurus
980	2	5.9	38	1	COA3_XANCP	Q07484	xanthomonas
981	2	5.9	38	1	CRS3_NOTGO	P15534	nototodarus
982	2	5.9	38	1	CU47_LACCU	P80323	lactobacill
983	2	5.9	38	1	DCHS_MICSP	P00863	micrococcus
984	2	5.9	38	1	DEF4_LEIQH	P41965	leiurus qui
985	2	5.9	38	1	DEF7_SPIOL	P81573	spinacia ol
986	2	5.9	38	1	DEF1_AESCY	P80154	aeschna cya

987	2	5.9	38	1	DEF1_MYTGA	P80571 mytilus gal
988	2	5.9	38	1	DLP3_ORNAN	P82141 ornithorhyn
989	2	5.9	38	1	DNP_DENAN	P28374 dendroaspis
990	2	5.9	38	1	DPOB_BOVIN	Q27958 bos taurus
991	2	5.9	38	1	E2F1_RAT	O09139 rattus norv
992	2	5.9	38	1	EST5_DROMO	P10095 drosophila
993	2	5.9	38	1	EXE1_HEL SU	P04203 heloderma s
994	2	5.9	38	1	FER_METPR	P81542 metallospha
995	2	5.9	38	1	GLUM_HYDCO	P23063 hydrolagus
996	2	5.9	38	1	GME1_RAT	Q9quz8 rattus norv
997	2	5.9	38	1	H5_COLLI	P02260 columba liv
998	2	5.9	38	1	HIS1_MACFA	P34084 macaca fasc
999	2	5.9	38	1	HMG2_BOVIN	P40673 bos taurus
1000	2	5.9	38	1	HOXH_RHOOP	P22661 rhodococcus

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.

AC P81175;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).

OS Rhamdia sapo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Pimelodidae; Rhamdia.

OX NCBI_TaxID=55673;

RN [1]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=98036128; PubMed=9370361;

RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,

RA Santome J.A.;

RT "Amino acid sequence, binding properties and evolutionary

RT relationships of the basic liver fatty-acid-binding protein from the

RT catfish Rhamdia sapo.";

RL Eur. J. Biochem. 249:510-517(1997).

CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: INTESTINE.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

DR InterPro; IPR000463; Fatty_acid_BP.

DR PROSITE; PS00214; FABP; PARTIAL.

KW Transport; Lipid-binding.

FT NON_TER 1 1

FT NON_CONS 12 13

FT NON_CONS 20 21

FT NON_CONS 28 29

FT NON_TER 33 33

SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 14.7%; Score 5; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
|||||
Db 13 SVSEI 17

RESULT 2

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
AC P11530;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dystrophin (Fragment).
GN DMD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122671; PubMed=3340214;
RA Nudel U., Robzyk K., Yaffe D.;
RT "Expression of the putative Duchenne muscular dystrophy gene in
RT differentiated myogenic cell cultures and in the brain.";
RL Nature 331:635-638(1988).
CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
CC plasma membrane.
CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
CC and SNTG2 (By similarity).
CC -----
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CC -----
DR EMBL; X07000; CAA30057.1; -.
DR PIR; S01614; S01614.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR PROSITE; PS00019; ACTININ_1; PARTIAL.
DR PROSITE; PS00020; ACTININ_2; PARTIAL.
DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 3

PCG3_PACGO

ID PCG3_PACGO STANDARD; PRT; 30 AA.
AC P82416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G3.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKGK 13
|||
Db 7 NKGK 10

RESULT 4

PSBY_SYNY3

ID PSBY_SYNY3 STANDARD; PRT; 39 AA.
AC P73676;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II protein Y.
GN PSBY OR SML0007.

OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 CC -!- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE
 CC METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM
 CC II (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CELLULAR THYLAKOID MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE PSBY FAMILY.
 CC -----
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 CC -----
 DR EMBL; D90908; BAA17722.1; -.
 DR PIR; S77164; S77164.
 KW Photosystem II; Transmembrane; Thylakoid; Complete proteome.
 FT TRANSMEM 5 25 POTENTIAL.
 SQ SEQUENCE 39 AA; 4202 MW; 3EA176ABAA79F6DF CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQDV 31
 ||||
 Db 31 LQDV 34

RESULT 5

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
 AC P08377;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sarcotoxin IC.
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7386;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=85207747; PubMed=3888997;
 RA Okada M., Natori S.;
 RT "Primary structure of sarcotoxin I, an antibacterial protein induced
 RT in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.";
 RL J. Biol. Chem. 260:7174-7177(1985).
 CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
 CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
 CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
 DR PIR; C22625; CKFHCS.
 DR InterPro; IPR000875; Cecropin.
 DR InterPro; IPR003253; Sarctxn_cecrpn.
 DR Pfam; PF00272; cecropin; 1.
 DR ProDom; PD001670; Sarctxn_cecrpn; 1.
 DR PROSITE; PS00268; CECROPIN; 1.
 KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
 FT MOD_RES 39 39 AMIDATION.
 SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 WLRK 26
 ||||
 Db 2 WLRK 5

RESULT 6

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
 AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROL OR GROEL OR MOPA.
 OS *Mycobacterium smegmatis*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved *Mycobacterium smegmatis*.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chaperonin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 18 LNS 20

RESULT 7

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
 AC P80499;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Kruff V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 of the protein complexes of plant mitochondria."
 RL Plant J. 9:357-368(1996).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 8

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases."
 RL FEBS Lett. 414:359-361(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
 |||
 Db 7 EWL 9

RESULT 9

OMPA_YERPS

ID OMPA_YERPS STANDARD; PRT; 28 AA.
 AC P38399;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Outer membrane protein A (Outer membrane protein II) (Fragment).
 GN OMPA.
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.

OX NCBI_TaxID=633;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90038529; PubMed=2478630;
 RA Zhang J.J., Hamachi M., Hamachi T., Zhao Y.P., Yu D.T.Y.;
 RT "The bacterial outer membrane protein that reacts with anti-HLA-B27
 RT antibodies is the OmpA protein.";
 RL J. Immunol. 143:2955-2960(1989).
 CC -!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
 CC SOLUTES (BY SIMILARITY).
 CC -!- SUBUNIT: Monomer (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
 DR PIR; A60752; A60752.
 DR HSSP; P02934; 1QJP.
 DR InterPro; IPR006690; OMPA_LIKE.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF01389; OmpA_membrane; 1.
 DR PROSITE; PS01068; OMPA; PARTIAL.
 KW Conjugation; Outer membrane; Transmembrane; Phage recognition; Porin.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3281 MW; E89F7526254B1E0E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKG 12
 |||
 Db 26 NKG 28

RESULT 10

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
 AC P20260;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
 DE 2-acylhydrolase) (Fragment).
 OS Pseudechis porphyriacus (Red-bellied black snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudechis.
 OX NCBI_TaxID=8671;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=89388835; PubMed=2675391;
 RA Schmidt J.J., Middlebrook J.L.;
 RT "Purification, sequencing and characterization of pseudexin
 RT phospholipases A2 from Pseudechis porphyriacus (Australian
 RT red-bellied black snake).";

RL Toxicon 27:805-818(1989).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
 CC SUBFAMILY.
 DR PIR; C32416; C32416.
 DR HSSP; P00592; 2PHI.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAAE0D5 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
 |||
 Db 3 IQL 5

RESULT 11

SCX2_BUTSI

ID SCX2_BUTSI STANDARD; PRT; 28 AA.
 AC P15230;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Peptide II.
 OS Buthus sindicus (Scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Mesobuthus.
 OX NCBI_TaxID=42519;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90060332; PubMed=2583272;
 RA Fazal A., Beg O.U., Shafqat J., Zaidi Z.H., Joernvall H.;
 RT "Characterization of two different peptides from the venom of the
 RT scorpion Buthus sindicus."
 RL FEBS Lett. 257:260-262(1989).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 DR PIR; S06668; S06668.
 DR HSSP; Q9NJP7; 1DU9.
 SQ SEQUENCE 28 AA; 2968 MW; 2EA9AD78BD39A3B8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 11 KGK 13

RESULT 12

SLP1_LEIQH

ID SLP1_LEIQH STANDARD; PRT; 28 AA.

AC P80669;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leiuropeptide I.

OS Leiurus quinquestriatus hebraeus (Yellow scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Buthoidea; Buthidae; Leiurus.

OX NCBI_TaxID=6884;

RN [1]

RP SEQUENCE, AND STRUCTURE BY NMR.

RC TISSUE=Venom;

RX MEDLINE=97411504; PubMed=9266482;

RA Buisine E., Wieruszeski J.-M., Lippens G., Wouters D., Tartar A.,

RA Sautiere P.;

RT "Characterization of a new family of toxin-like peptides from the

RT venom of the scorpion Leiurus quinquestriatus hebraeus. 1H-NMR

RT structure of leiuropeptide II.";

RL J. Pept. Res. 49:545-555(1997).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.

DR HSSP; Q9NJP7; 1DU9.

KW Toxin.

FT DISULFID 3 19

FT DISULFID 6 24

FT DISULFID 10 26

SQ SEQUENCE 28 AA; 2954 MW; 5F72AD78BD39BE1B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 11 KGK 13

RESULT 13

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.

AC P48142; P01285;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Vasoactive intestinal peptide (VIP).

GN VIP.

OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 14

VIP_RANRI
 ID VIP_RANRI STANDARD; PRT; 28 AA.
 AC P81016;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH

CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 15

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.
 AC P04565;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Ovis aries (Sheep),
 OS Capra hircus (Goat), and
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940, 9925, 9615;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Brain;
 RX MEDLINE=91045331; PubMed=2235680;
 RA Gafvelin G.;
 RT "Isolation and primary structure of VIP from sheep brain.";
 RL Peptides 11:703-706(1990).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Small intestine;
 RX MEDLINE=91239834; PubMed=2034821;
 RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
 RA Christophe J.;
 RT "Purification and amino acid sequence of vasoactive intestinal
 RT peptide, peptide histidine isoleucinamide and secretin from the ovine
 RT small intestine.";
 RL Regul. Pept. 32:169-179(1991).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=C.hircus, and C.familiaris;
 RX MEDLINE=86313167; PubMed=3748846;
 RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;

RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A60304; A60304.
DR PIR; B60072; VRSH.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 16

CXOC_CONMA

ID CXOC_CONMA STANDARD; PRT; 29 AA.
AC P37300;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-conotoxin MVIIC precursor (SNX-230) (Fragment).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS.
RX MEDLINE=92337922; PubMed=1352986;
RA Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
RA Cruz L.J., Imperial J.S., Olivera B.M.;
RT "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
RL Neuron 9:69-77(1992).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=95248539; PubMed=7731037;
RA Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
RA Basus V.J.;
RT "Solution structure of omega-conotoxin MVIIC, a high affinity ligand
RT of P-type calcium channels, using 1H NMR spectroscopy and complete
RT relaxation matrix analysis.";

RL J. Mol. Biol. 248:106-124(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99303703; PubMed=10373375;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [4]
 RP MUTAGENESIS OF TYR-15.
 RX MEDLINE=95408251; PubMed=7677735;
 RA Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
 RA Sato K.;
 RT "Tyr13 is essential for the binding of omega-conotoxin MVIIC to the
 RT P/Q-type calcium channel.";
 RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels as well as types of high-threshold
 CC voltage-gated calcium channels resistant to both dihydropyridines
 CC and omega-conotoxin GVIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; S40826; AAB22674.1; -.
 DR PIR; JH0699; JH0699.
 DR PDB; 1OMN; 01-DEC-95.
 DR PDB; 1CNN; 31-MAY-00.
 KW Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
 KW Calcium channel inhibitor; Hydroxylation; Amidation; 3D-structure.
 FT NON_TER 1 1
 FT PROPEP <1 2
 FT PEPTIDE 3 28 OMEGA-CONOTOXIN MVIIC.
 FT BINDING 15 15 ESSENTIAL FOR CALCIUM CHANNEL BINDING.
 FT DISULFID 3 18
 FT DISULFID 10 22
 FT DISULFID 17 28
 FT MOD_RES 9 9 HYDROXYLATION (PROBABLE).
 FT MOD_RES 28 28 AMIDATION (G-29 PROVIDE AMIDE GROUP).
 FT MUTAGEN 15 15 Y->A: HIGH DECREASE IN BINDING.
 FT TURN 6 7
 FT STRAND 9 9
 FT HELIX 12 14
 FT TURN 24 25
 FT STRAND 27 27
 SQ SEQUENCE 29 AA; 3071 MW; AC7A68948474728A CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 4 KGK 6

RESULT 17

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
AC P47215;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95023390; PubMed=7524049;
RA Wang Y., Conlon J.M.;
RT "Purification and primary structure of galanin from the alligator
RT stomach.";
RL Peptides 15:603-606(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 18

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS *Amia calva* (Bowfin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; *Amia*.
 OX NCBI_TaxID=7924;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95083480; PubMed=7527531;
 RA Wang Y., Conlon J.M.;
 RT "Purification and characterization of galanin from the
 RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
 RT (*Scyliorhinus canicula*).";
 RL Peptides 15:981-986(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

 Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 19

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
 AC P30802;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS *Gallus gallus* (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC *Gallus*.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;

RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC !- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 20

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC !- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC !- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 21

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase."
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||

Db

4 LNS 6

RESULT 22

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
AC P31234;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
GN GAL OR GALN OR GLNN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92158824; PubMed=1724081;
RA Sillard R., Langel U., Joernvall H.;
RT "Isolation and characterization of galanin from sheep brain.";
RL Peptides 12:855-859(1991).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PRINTS; PR00273; GALANIN.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17

|||

Db 4 LNS 6

RESULT 23

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.
AC P31297;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon.
GN GCG.

OS Chinchilla brevicaudata (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
 OC Chinchilla.
 OX NCBI_TaxID=10152;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91045327; PubMed=2235678;
 RA Eng J., Kleinman W.A., Chu L.S.;
 RT "Purification of peptide hormones from chinchilla pancreas by
 RT chemical assay.";
 RL Peptides 11:683-685(1990).
 CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
 CC THE BLOOD SUGAR LEVEL.
 CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60413; GCCB.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone.
 SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15
 |||
 Db 12 KHL 14

RESULT 24

IPYR_DESVH
 ID IPYR_DESVH STANDARD; PRT; 29 AA.
 AC P19371;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase) (Fragment).
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme.";
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).

CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 25

NUO1_SOLTU

ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=41113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
 RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT Solanum tuberosum."
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29

SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKK 27
|||
Db 2 RKK 4

RESULT 26

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
|||
Db 11 EWL 13

RESULT 27

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7P (Fragment).

GN RPS7P OR S7.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens.";
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 28

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.
 AC P80740;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
 DE V) (Fragment).
 OS Olea europaea (Common olive).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea.";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.
 DR Pfam; PF00080; sodcu; 1.
 DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 7 LNS 9

RESULT 29

TL16_SPIOL

ID TL16_SPIOL STANDARD; PRT; 29 AA.

AC P81834;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI_TaxID=3562;

RN [1]

RP SEQUENCE.

RC TISSUE=Leaf;

RX MEDLINE=98175931; PubMed=9506969;

RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;

RT "The thylakoid lumen of chloroplasts. Isolation and

RT characterization.";

RL J. Biol. Chem. 273:6710-6716(1998).

CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.

KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 30

CY35_DESAC

ID CY35_DESAC STANDARD; PRT; 30 AA.
AC P81079;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c3, 50 kDa (Fragment).
OS Desulfuromonas acetoxidans (Chloropseudomonas ethylica).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Desulfuromonadaceae; Desulfuromonas.
OX NCBI_TaxID=891;
RN [1]
RP SEQUENCE.
RX MEDLINE=97419123; PubMed=9271490;
RA Bruschi M., Woudstra M., Guigliarelli B., Asso M., Lojou E.,
RA Petillot Y., Abergel C.;
RT "Biochemical and spectroscopic characterization of two new
RT cytochromes isolated from Desulfuromonas acetoxidans.";
RL Biochemistry 36:10601-10608(1997).
CC -!- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
CC DEHYDROGENASE TO FERREDOXIN. THE REDOX POTENTIALS OF THIS
CC CYTOCHROME ARE -140 MV, -210 MV AND -240 MV.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- PTM: BINDS 4 HEMES.
CC -!- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
DR InterPro; IPR000345; CytC_heme_bind.
DR PROSITE; PS00190; CYTOCHROME_C; PARTIAL.
KW Electron transport; Sulfate respiration; Heme; Periplasmic.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3018 MW; B0D52603DD5069B8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 15 KGK 17

RESULT 31

DMS3_PHYSA
 ID DMS3_PHYSA STANDARD; PRT; 30 AA.
 AC P80279;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dermaseptin 3 (DS III).
 OS Phyllomedusa sauvagei (Sauvage's leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8395;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=94139686; PubMed=8306981;
 RA Mor A., Nicolas P.;
 RT "Isolation and structure of novel defensive peptides from frog skin.";
 RL Eur. J. Biochem. 219:145-154(1994).
 CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
 CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
 CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Dermaseptin subfamily.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
 SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
 |||
 Db 23 KKL 25

RESULT 32

FTN_BACFR
 ID FTN_BACFR STANDARD; PRT; 30 AA.
 AC P28733;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from Bacteroides fragilis.";
 RL FEMS Microbiol. Lett. 74:207-212(1992).

CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 33

GLUM_ANGAN

ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glucagon-like peptide (GLP).
 OS Anguilla anguilla (European freshwater eel), and
 OS Anguilla rostrata (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.anguilla, and A.rostrata;
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;
 RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, Anguilla rostrata and the
 RT European eel, Anguilla anguilla."
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Amidation.
FT MOD_RES 30 30 AMIDATION.
SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30
|||
Db 14 LQD 16

RESULT 34

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.
AC P11726;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
DE (Fragment).
OS Aeromonas punctata (Aeromonas caviae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 9232;
RX MEDLINE=85104799; PubMed=3968036;
RA Falmagne P., Portetelle D., Stalon V.;
RT "Immunological and structural relatedness of catabolic ornithine
RT carbamoyltransferases and the anabolic enzymes of enterobacteria."
RL J. Bacteriol. 161:714-719(1985).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
DR InterPro; IPR006130; Asp/Orn_Cotranf.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF02729; OTCace_N; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
|||
Db 19 EIQ 21

RESULT 35

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
AC P82415;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G2.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KGK 13
|||
Db 8 KGK 10

RESULT 36

TX2_THRPR

ID TX2_THRPR STANDARD; PRT; 30 AA.
AC P83476;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toxin ProTx-II.
OS Thrixopelma pruriens (Green velvet).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Theraphosidae; Thrixopelma.
OX NCBI_TaxID=213387;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=22363233; PubMed=12475222;
RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,

RA Mehl J.T., Cohen C.J., Smith M.M.;
 RT "Two tarantula peptides inhibit activation of multiple sodium
 channels.";
 RL Biochemistry 41:14734-14747(2002).
 CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
 CC Shifts the voltage-dependence of channel activation to more
 CC positive potentials.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
 CC TOXIN FAMILY.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
 KW Sodium channel inhibitor.
 FT DISULFID 2 16
 FT DISULFID 9 21
 FT DISULFID 15 25
 SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

 Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 26 KKL 28
 |||
 Db 27 KKL 29

RESULT 37
 UP61_UPEIN
 ID UP61_UPEIN STANDARD; PRT; 30 AA.
 AC P82037;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 6.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 38

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
AC P82038;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.2.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 39

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
AC Q04238;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
DE (Fragment).
OS Equisetum arvense (Field horsetail) (Common horsetail).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
 OX NCBI_TaxID=3258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93138084; PubMed=8422915;
 RA Starke T., Gogarten J.P.;
 RT "A conserved intron in the V-ATPase A subunit genes of plants and
 RT algae.";
 RL FEBS Lett. 315:252-258(1993).
 CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
 CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
 CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
 CC CELLS.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
 CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
 CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
 CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
 CC V-ATPASE SUBUNIT IN PSILLOTUM AND EQUISETUM.
 CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
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 DR EMBL; X56984; CAA40302.1; -.
 DR PIR; S21815; S21815.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
 KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
 KW Multigene family.
 FT NON_TER 1 1
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 MER 20
 |||
 Db 23 MER 25

RESULT 40
 Y523_BORBU
 ID Y523_BORBU STANDARD; PRT; 30 AA.
 AC 051473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein BB0523.
 GN BB0523.
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia*
 RT *burgdorferi*.";
 RL Nature 390:580-586(1997).
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 CC -----
 DR EMBL; AE001154; AAC66894.1; -.
 DR PIR; B70165; B70165.
 DR TIGR; BB0523; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 26 ERV 28

Search completed: January 14, 2004, 10:35:33
 Job time : 7.61371 secs